```
November 18, 2002, 11:30:36; Search time 35 Seconds (without alignments) 2278.292 Million cell updates/sec
                                                                                                                                             US-09-895-913A-120
387
1 MIPKERMERALGSGVIISKD......RPKRFLVLDLNQGYRIILVK 387
                                                                                                                                                                                                                                                                                                                   671580
GenCore version 5.1.3
Copyright (c) 1993 - 2002 Compugen Ltd.
                                                                                                                                                                                                                                                                                                                 Total number of hits satisfying chosen parameters:
                                                                                                                                                                                                                                                       671580 seqs, 206047115 residues
                                                           OM protein - protein search, using sw model
                                                                                                                                                                                                                                                                                                                                                                                          Post-processing: Listing first 45 summaries
                                                                                                                                                                                                            OLIGO
Gapop 60.0 , Gapext 60.0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                  sp_fung1:*
sp_human:*
sp_huvertebrate:*
sp_mammal:*
sp_mhc:*
sp_pragnelle:*
sp_phage:*
sp_phage:*
sp_rodent:*
sp_rodent:*
sp_rodent:*
sp_rodent:*
sp_virus:*
sp_virus:*
                                                                                                                                                                                                                                                                                                                                                                                                                      SPTREMBL_21:*
1: sp_archea:*
2: sp_bacteria:*
                                                                                                                                                                                                                                                                                                                                               Minimum DB seq length: 0
Maximum DB seq length: 2000000000
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 55...
111...
112...
114...
115...
                                                                                                                                                                                                                                                                                   0
                                                                                                                                                Title:
Perfect score:
Sequence:
                                                                                                                                                                                                            Scoring table:
                                                                                                                                                                                                                                                                                   Word size :
                                                                                                                                                                                                                                                                                                                                                                                                                      Database :
                                                                                                                                                                                                                                                       Searched:
                                                                                       Run on:
```

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

sp_unclassified:*
sp_rvirus:*
sp_bacteriap:*
sp_archeap:*

SUMMARIES

			•	Š	•												
	Description	025663 helicobacte	Q9zm18 helicobacte	Q46094 campylobact 4	Q46120 campylobact	Q9pn69 campylobact	O31388 bradyrhizob	Q9pql3 xylella fas	Q8ue46 agrobacteri	Q97lul clostridium	Q8r6v1 thermoanaer	Q93j30 streptomyce	099td6 staphylococ	O68197 haemophilus	Q56885 yersinia en 🌑	Q44596 brucella ab	Q8yhl4 brucella me
	ID	025663	Q92M18	046094	046120	69N460	031388	Q9PGL3	Q8UE46	Q97LU1	Q8R6V1	093J30	Q99TD6	068197	056885	Q44596	O8YHL4
	DB	16	16	~	~	16	7	16	16	16	16	16	16	N	~	7	16
	Query Match Length DB	443	476	368	472	472	371	481	495	348	367	519	424	437	464	474	474
æ	Query Match	100.0	24.8	5.2	5.2	5.2	4.7	4.7	4.4	3.6	3.6	3.4	3.1	3.1	3.1	3.1	3.1
	Score	387	96	20	20	20	18	18	17	14	14	13	12	12	12	12	12
	Result No.	-	2	m	4	S	9	7	80	6	10	11	12	13	14	15	16

Q829b0 salmonella Q8rss1 klebsiella P74978 yersinia en Q8zhm6 yersinia pe	ば	H 0	Q92ey8 listeria in Q8ya67 listeria mo Q9an listeria mo Q9an listeria mo Q9an streptomyce Q9ed67 mycobacteri	Q51374 pseudomonas Q9hvx1 pseudomonas Q8xv99 ralstonia s Q985r6 bacillus ha	
Q8Z9B0 Q8RSS1 P74978 Q8ZBM6	Q98N31 Q9R756 Q9FD11 Q8ZL01	Q8Z3E6 Q8X9F1 Q8ZB58 Q06439	292EY8 Q92EY8 Q8YA67 Q9CMR4 Q9S2R5	Q51374 Q9HVX1 Q8XV99 Q9K5R6 Q9SKG9	Q8VKA4 Q9Z5G6 Q9KUF5 O53896 Q92Z82
16 16 16	16 16 16 16	16 16 2	16 16 16 16	2 16 16	16 16 16 16
475 477 478 481	4 4 4 4 5 4 4 5 5 3 4 5 5 5 5 5 5 5 5 5	455 455 457 460	3 3 3 5 5 5 5 5 5 5 5 5 5 5 5 5 5 5 5 5	389 403 406 704	4 4 4 5 6 4 6 4 6 8 4 6 8 4 6 8 8 8 8 8 8 8 8 8
	9 6 6 6 6	44444 88888	3000000	00000 00000	00000
122	1222	11111	111000	00000	010101
17 18 19 20	22222	755 756 766 766 766	3 8 8 8 8 8 8 8 8 8 8 8 8 8 8 8 8 8 8 8	337 409 409	4 4 4 4 4 11 4 5 4 5 5

ALIGNMENTS

```
SMART; SM00228; PDZ; 2.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Matches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                RESULT 4
Q46120
ID Q461
AC Q461
                                                                                                                                                                                                                                                                                                                                                                                                                                               046094
  DR DR SO SO
                                                                                                                                                                                                                                                                   g
                                                                                                                                                                                                                                                                                                                                                   엄
                                                                                                                                                                                                                                                                                                              ö
                                                                                                                                                                                                                         à
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ACCOCCOS OCT TO THE STANT TO TH
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  g
                                                                                                                                                                                                  ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             SEQUENCE FROM N.A.
MEDLINE-99120557; PubMed=9923682;
Alm R.A., Ling L.-S.L., Moir D.T., King B.L., Brown E.D., Doig P.C.,
Smith D.R., Noonan B., Guild B.C., deJonge B.L., Carmel G.,
Tummino P.J., Caruso A., Uria-Nickelsen M., Mills D.M., Ives C.,
Gibson R., Merberg D., Mills S.D., Jiang Q., Taylor D.E., Vovis G.F.,
                                                                                                                                                                                                                                                                61 AVIRITKDNLPTIKFSDSNDISVGDLVFAIGNPFGVGESVTQGIVSALNKSGIGINSYEN 120
                                                                                                                                                                                                                                                                                                                                                                                                                     121 FIQTDASINPGNSGGALIDSRGGLVGINTAIISKTGGNHGIGFAIPSNMVKDTVTQLIKT 180
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          GKIERGYLGVGLQDLSGDLQNSYDNKEGAVVISVEKDSPAKKAGILVWDLITEVNGKKVK 240
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    OVEDLTQETKRSMRLSDDVQGVLVSQVNENSPAEQAGFRQGNIITKIEEVEVKSVADFNH 360
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Gaps
                                                                                                                                                                                                                                            1 MIPKERMERALGSGVIISKDGYIVTNNHVIDGADKIKVTIPGSNKEYSATLVGTDSESDL 60
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      'Genomic sequence comparison of two unrelated isolates of the human
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Helicobacter pylori J99 (Campylobacter pylori J99).
Bacteria; Proteobacteria; epsilon subdivision; Helicobacter group;
                                                                                                                                                                                                                                                                                                                                                                                                                                          ;
0
                                                                                                                                                     DB 16; Length 443;
                PROSITE; PS50106; PD2; 2.
PROSITE; PS50240; TRYPSIN_DOM; 1.
Hydrolase; Hypothetical protein; Protease; Serine protease;
                                                                                                                                                                                                Indels
                                                                                                         03FDDBD72CF31EE2 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        gastric pathogen Helicobacter pylori.";
Nature 397.176-180(1999).
-i- SIMILARITY: TO SERINE PROTEASES, TRYPSIN FAMILY
EMBL: AE001474; AAD05980.1; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     01-WAY-1999 (TrEMBLrel. 10, Created)
01-WAY-1999 (TrEMBLrel. 10, Last sequence update)
01-JUN-2002 (TrEMBLrel. 21, Last annotation update)
                                                                                                                                                                                                ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                476 AA
                                                                                                                                              Query Match 100.0%; Score 387; D Best Local Similarity 100.0%; Pred. No. 0; Matches 387; Conservative 0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             MEROPS; S01.273; -...
InterPro: IPR001478; PDZ.
InterPro: IPR0011940; Protease2C.
InterPro: IPR001254; Ser_protease_Try.
Pfam; PF00595; PDZ; 1.
Pfam; PF00899; tryps1n; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  361 ALEKYKGKPKRFLVLDLNQGYRIILVK 387
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  PRT;
                                                                                                       443 AA; 47983 MW;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           PRINTS; PRO0834; PROTEASES2C.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                PRELIMINARY;
SMART; SM00228; PDZ; 2.
                                                                                    Complete proteome. SEQUENCE 443 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     NCBI_TaxID-85963;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Protease DO.
HTRA OR JHP0405.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Helicobacter
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Trust T.J.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              09ZM18;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          181
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    301
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  RESULT O
DR DR DR SO KW
                                                                                                                                                                                                                                                                                   a
                                                                                                                                                                                                                                                                                                                              ò
                                                                                                                                                                                                                                                                                                                                                                        g
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      g
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               셤
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ò
                                                                                                                                                                                                                                                                                                                                                                                                                     õ
                                                                                                                                                                                                                                                                                                                                                                                                                                                          q
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ò
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               g
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ò
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    å
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ö
```

```
ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ö
                                                                                                                                                                                                   174 VTQLIKTGKIERGYLGVGLQDLSGDLQNSYDNKEGAVVISVEKDSPAKKAGILVWDLITE 233
                                                                                                                                                                                                                        263 VTQLIKTGKIERGYLGVGLQDLSGDLQNSYDNKEGAVVISVEKDSPAKKAGILVWDLITE 322
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Gaps
                                                                                                                                                          Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Campylobacter jejuni.
Bacteria; Proteobacteria; epsilon subdivision; Campylobacter group;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Taylor D.E., Hiratsuka K.; use of non-radioactive DNM probes for detection of Campylobacter jejuni and Campylobacter coli in stool specimens."; Moi. Cell. Probes 4:261-271(1990).
                                                                                                                                                       ó
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ö
                                                                                                            Length 476;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Length 368
                                                                                                                                                       Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Submitted (MAY-1995) to the EMBL/GenBank/DDBJ databases EMBL; U27271; AAA68943.1; -.
PROSITE; PS50106; PDZ; 2.
PROSITE; PS50240; TRYPSIN_DOM; 1.
Hydrolase; Serine protease; Complete protecome.
Hydrolase; 51713 MW; 4E338AED839BFE18 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        368 AA; 39491 MW; CFA14B08EE49EF70 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     01-NOV-1996 (TrEMBLrel. 01, Created)
01-NOV-1996 (TrEMBLrel. 01, Last sequence update)
01-MAR-2002 (TrEMBLrel. 20, Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Score 20; DB 2; Len
Pred. No. 9.5e-13;
                                                                                                         DB 16; L
7.5e-96;
hes 0;
                                                                                                                                                                                                                                                                                        234 VNGKKVKNTNELRNLIGSMLPNQRVTLKVIRDKKER 269
                                                                                                                                                                                                                                                                                                               323 VNGKKVKNTNELRNLIGSMLPNQRVTLKVIRDKKER 358
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Heat shock protein/serine protease (Fragment)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 472 AA
                                                                                                         24.8%; Score 96; DB 100.0%; Pred. No. 7.5 ive 0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  5.2%; Score 20; DB 100.0%; Pred. No. 9.5 tive 0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    InterPro; IPR01478; PD2.
InterPro; IPR01940; Protease2C.
InterPro; IPR001254; Ser_protease_Try.
Pfam; PF00595; PD2; 2.
Pfam; PF00089; trypsin; 1.
PRINTS; PR00834; PROTEASES2C.
SMART; SM00228; PD2; 2.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               PROSITE; PSS0106; PD2; 1.
PROSITE; PSS0106; TRYPSIN DOM; 1.
Hydrolase; Protease; Serine protease.
NON TER
SEQUENCE 368 AA; 39491 MW; CFA14B
                                                                                                                                                                                                                                                                                                                                                                                                                                              PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     STRAIN-UA580;
MEDLINE-90384493; PubMed-2402249;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         118 YENFIQTDASINPGNSGGAL 137
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   106 YENFIQTDASINPGNSGGAL 125
                                                                                                       Query Match
Best Local Similarity 100.0
Matches 96; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                              PRELIMINARY;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                20; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 PRELIMINARY;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Query Match
Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          SEQUENCE FROM N.A.
STRAIN-UA580;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      MEROPS; S01.273; -
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    NCBI_TaxID-197;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Campylobacter
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Hiratsuka K.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                     046094;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               046120
Q46120;
                                                                                                                                                                                                                                                                                                                                                                                                                                              046094
```

```
SMART; SM00228; PDZ; 2.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Heat shock protein.
XF0285.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Sest Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             MEROPS; S01.274; -
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Xylella fastidiosa
                                                                                                                                                                                                                             Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            NCBI_TaxID=375
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    DegP protein.
                                                                                                                                                                                                Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  031388
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Q9PGL3
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Matches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      RESULT 6
031388
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        RESULT 7
Q9PGL3
      DR DR DR SO SO
                                                                                                                                                                                                                                                                                                                          οý
                                                                                                                                                                                                                                                                                                                                                                                         a
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ACCOCCOS NO COCCOS NO COCC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ò
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Dp
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ó
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     PERMINICATE 11168;
MEDIATRE-2012; PubMed=10688204;
MEDIATRE-2012; PubMed=10688204;
MEDIATRE-2012; PubMed=10688204;
Bashall J. Wren B.W., Mungall K., Ketley J.M., Churcher C.,
Basham D., Chillingworth T., Davies R.M., Feltwell T., Holroyd S.,
Jagels K., Karlyshev A.V., Moule S., Pallen M.J., Penn C.W.,
Ouail M.A., Rajandream M.A., Rutherford K.M., van Vliet A.H.M.,
Whitehead S., Barrell B.G.,
The genome sequence of the food-borne pathogen Campylobacter jejuni
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Gaps
                                                                                                                                                           Campylobacter jejuni.
Bacteria; Proteobacteria; epsilon subdivision; Campylobacter group;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Campylobacter jejuni.
Bacteria; Proteobacteria; epsilon subdivision; Campylobacter group;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     .;
0
                                                                                                                                                                                                                                                                                                                                                                                   Henderson J., Wood A.C., Emery M.J., Wren B.W., Ketley J.; "Characterisation of a Campylobacter jejuni high-temperaturerequirement A (htrA) isogenic mutant."; Submitted (MAY-1997) to the EMBL/GenBank/DDBJ databases. EMBL; X82628; CAA57948.1; -
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Ouery Match 5.2%; Score 20; DB 2; Length 472; Best Local Similarity 100.0%; Pred. No. 1.2e-12; Matches 20; Conservative 0; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             PROSITE: PS50106; PD2: 1.
PROSITE; PS50240; TRYPSIN_DOM: 1.
Hydrolase; Protease: Serine protease.
SEQUENCE 472 AA: 50941 MW; 0C16E381E97424D1 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     reveals hypervariable sequences.";
Nature 403:665-668(2000).
-i- SIMILARITY: TO SERINE PROTEASES, TRYPSIN FAMILY
EMBL; AL139077; CAB73482.1;
01, Created)
04, Last sequence update)
20, Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       01-OCT-2000 (TrEMBLrel. 15, Created)
01-OCT-2000 (TrEMBLrel. 15, Last sequence update)
01-MAR-2002 (TrEMBLrel. 20, Last annotation update)
Serine protease (protease DO) (EC 3.4.21.).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  InterPro; IPR001478; PDZ.
InterPro; IPR001940; Protease2C.
InterPro; IPR001954; Ser_protease_Try.
Pfan; PP00595; PDZ; 2.
Pfan; PP00089; trypsin; 1.
PKINTS; PR00894; PROTEASES2C.
SWART; SW00228; PDZ; 2.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Interpro; IPR001478; PDZ.
InterPro; IPR001940; Protease2C.
InterPro; IPR001254; Ser_protease_Try.
Pfam; PF000595; PDZ; Z.
Pfam; PF000695; trypsin; 1.
PRINTS; PR00834; PROTEASES2C.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  210 YENFIQTDASINPGNSGGAL 229
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                118 YENFIQTDASINPGNSGGAL 137
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              PRELIMINARY;
                             01-JUL-1997 (TrEMBLrel. 01-MAR-2002 (TrEMBLrel.
   (TrEMBLrel.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  MEROPS; S01.273; -
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                          SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      MEROPS; S01.273;
                                                                                                Serine protease.
                                                                                                                                                                                                                                                        NCBI_TaxID=197;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        HTRA OR CJ1228C
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               NCBI_TaxID=197;
                                                                                                                                                                                                                          Campylobacter
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Campylobacter
   01-NOV-1996
01-JUL-1997
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              69NG60
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                RESULT 5
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    09PN69
      DDT REP BY COCC ON THE BY COCC ON TH
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            d
```

```
ö
                                                                                                                                                                                ö
                                                                                                                                                                                  Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        part of
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Bradyrhizobium japonicum.
Bacteria; Protecbacteria; alpha subdivision; Rhizobiaceae group;
Bradyrhizobium group; Bradyrhizobium.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Bacteria; Proteokacteria; gamma subdivision; Xanthomonas group;
Xylella.
NCBI_TaxID=2371;
                                                                                                                                                                                ;
0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                MEDLINE-98114461; PubMed-9446679;
Narberhaus F., Weiglhofer W., Fischer H.M., Hennecke H.;
Narberhaus F., Weiglhofer W., Fischer H.M., Hennecke H.;
"Identification of the Bradyrhizobium japonicum degP gene as Jan operon containing small heat shock protein genes.";
Arch. Microbiol. 169:89-97(1998).
EMBL; X13616; CAA73938.1; -.
                                                                                                                        5.2%; Score 20; DB 16; Length 472; 100.0%; Pred. No. 1.2e-12; tive 0; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     4.7%; Score 18; DB 2; Length 371;
100.0%; Pred. No. 1.5e-10;
ive 0; Mismatches 0; Indels
PROSITE; PS50106; PDZ; 2.
PROSITE; PS50240; TRYPSIN.DOM; 1.
HYDROJASE; Serine profease; Complete proteome.
SEQUENCE 472 A3, 51006 MW; DCE4B51540E9894B CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Hydrolase; Serine protease.
SEQUENCE 371 AA; 39108 MW; 3CEIC77E17B86CDC CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                01-JAN-1998 (TrEMBLrel. 05, Created)
01-JAN-1998 (TrEMBLrel. 05, Last sequence update)
01-JUN-2002 (TrEMBLrel. 21, Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Last sequence update)
Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                481 AA
                                                                                                                                                                                                                                                                                                                                                                                                                  371 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        InterPro; IPR001478; PDZ.
InterPro; IPR001940; Protease2C.
InterPro; IPR001254; Ser_protease_Try.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Created)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          PROSITE; PS50106; PDZ; 1.
PROSITE; PS50240; TRYPSIN_DOM; 1.
                                                                                                                                                                                                                                                                210 YENFIQTDASINPGNSGGAL 229
                                                                                                                                                                                                                                  118 YENFIQTDASNNPGNSGGAL 137
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Pfam; PF00595; PDZ; 1.
Pfam; PF00089; trypsin; 1.
PRINTS; PR00834; PROTEASES2C.
SMART; SM00228; PDZ; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Q9PGL3;
01-OCT-2000 (TrENBLrel. 15,
01-OCT-2000 (TrENBLrel. 15,
01-MAR-2002 (TrENBLrel. 20,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                121 FIQTDASINPGNSGGALI 138
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          204 FIQTDASINPGHSGGALI 221
                                                                                                                                                                             Matches 20; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             18; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             PRELEMINARY;
                                                                                                                                                                                                                                                                                                                                                                                                                  PRELIMINARY;
```

```
Protease; Complete proteome
                                                                                                                                                                                                                                                                                                                                                                      SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                  Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Q97LU1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         CAC0463
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      097LU1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            RESULT 9
Q97LU1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 g
  à
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ö
                                REDLINE-2036/JT; Pubmed=10910347;

REDLINE-2036/JT; Pubmed=10910347;

RA Barros M.H., Bonacorsi E.D., Bordin S., Bove J.M., Barinsta C.S.,

RA Barros M.H., Bonacorsi E.D., Bordin S., Bove J.M., Barinses M.R.S.,

Buenco M.R.P., Camargo A.A., Camargo L.E.A., Carraro D.M., Carrar H.,

RA Collauto N.B., Colombo C., Costa F.P., Costa M.C.R., Costa P.D.

RA Collauto N.B., Colombo C., Costa F.P., Costa M.C.R., Costa P.D.

RA Collanto L.L., CITStoffani M., Dias-Neto E., Docena C., El-Dorry H.,

RA Fraga J.S., Franca S.C., Franco M.C., Frohme M., Furlan L.R.,

RA Fraga J.S., Franca E.C., Franco M.C., Frohme M., Fullan L.R.,

RA Fraga J.S., Mardena E.E., Langate E.L., Kitajima J.P.,

RA Krieger J.E., Kuramae E.E., Langes S.L., Copes S.L., Kitajima J.P.,

RA Machado M.A., Madeira A.M.B.N., Madeira H.M.F., Marino C.L.,

Mardues M.V., Martins E.A.L., Martins E.M.F., Martino C.L.,

Mardues M.V., Martins E.A.L., Martins E.M.F., Matsukuma A.Y.,

RA Machado M.A., Nagai M.A., Nascimento A.L.T.O., Netto L.E.S.,

RA Monn D.H., Nagai M.A., Nascimento A.L.T.O., Netto L.E.S.,

RA Monn J. Jr., Nobrega F.G., Munes L.R., Oliveira M.A.,

RA Goliveira M.C., de Oliveira R.C., Palmieri D.A., Paris A.J.,

RA Goliveira M.C., de Sa R.G., Santelli R.V., Savasaki H.E.,

RA Goliveira J.F., Silvestri M.L.Z., Siqueira W.J., de Souza A.A.,

RA de Souza A.P., Terenzi M.F., Truffi D., Tsai S.M., Tsuhako M.H.,

RA Zago M.A., Zatz M., Medanis J., Setubal J.C.;

RA Zago M.A., Zatz M., Medanis J., Setubal J.C.;

RA Zago M.A., Zatz M., Medanis J., Setubal J.C.;

REBL: Asdol3881.77. To SERNE PROTEASES, TRYPSIN FAMILY.

REBL: RADIABITY: TO SERNE PROTEASES, TRYPSIN FAMILY.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   [1]
SEQUENCE FROM N.A.
MEDLINE-21608550; PubMed-11743193;
Wood D.W., Setubal J.C., Kaul R., Monks D.E., Kitajima J.P.,
Wood D.W., Schou Y., Chen L., Wood G.E., Almeida N.F. Jr., Woo L.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Agrobacterium tumefaciens (strain C58 / ATCC 33970).
Bacteria; Proteobacteria; alpha subdivision; Rhizobiaceae group;
Rhizobiaceae; Rhizobium.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  .
0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     4.7%; Score 18; DB 16; Length 481;
100.0%; Pred. No. 1.9e-10;
Live 0; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               PROSITE; PS50106; PD2; 2.
PROSITE; PS50240; TRYPSIN_DOM; 1.
Hydrolase; Serine protesse; Complete proteome.
SEQUENCE 481 AA; 50526 MW; E90D291491D8EC18 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      01-JUN-2002 (TrEMBLrel. 21, Created)
01-JUN-2002 (TrEMBLrel. 21, Last sequence update)
01-JUN-2002 (TrEMBLrel. 21, Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             495 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                              InterPro; IPR001478; PDZ.
InterPro; IPR001478; PDZ.
InterPro; IPR001364; Ser_protease_Try.
Pfam; PF00595; PDZ; 1.
Pfam; PF00089; trypsin; 1.
PRINTS; PR00894; PROTEASES2C.
SMART; SM00228; PDZ; 2.
                           MEDLINE=20365717; PubMed=10910347;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 HTRA OR ATU1915 OR AGR_C_3507
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       222 NFIQTDASINPGNSGGAL 239
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           120 NFIQTDASINPGNSGGAL 137
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                18; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             PRELIMINARY;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        NCBI_TaxID-176299;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Serine protease.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Q8UE46
Q8UE46;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Matches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 RESULT 8
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Q8UE46
ò
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     q
```

```
REQUENCE FROM N.A.

SEQUENCE FROM N.A.

SEQUENCE FROM N.A.

SEQUENCE FROM N.A.

SEQUENCE FROM N.A.

MEDINE—21359325; bubmed—11466286;

RA

MEDINE—21359325; bubmed—11466286;

RA

Glbson R., Lee H.M., Dubois J., Qiu D., Hitti J., Wolf Y.I.,

RA

Glbson R., Lee H.M., Dubois J., Qiu D., Hitti J., Wolf Y.I.,

RA

Tatusov R.L., Sabathe F., Doucette-steamm L., Soucallle P., Daly M.J.,

RA

Tatusov R.L., Sabathe F., Doucette-steamm L., Soucallle P., Daly M.J.,

RA

Tatusov R.L., Sabathe F., Suborette-steamm L., Soucallle P., Daly M.J.,

RA

Tatusov R.L., Sabathe F., Soucette-steamm L., Soucallle P., Daly M.J.,

RA

Tatusov R.L., Sabathe F., Soucette-steamm L., Soucallle P., Daly M.J.,

RA

Tatusov R.L., Sabathe F., Soucette-steamm L., Soucallle P., Daly M.J.,

RA

Tatusov R.L., Sabathe F., Soucette-steamm L., Soucallle P., Daly M.J.,

RA

Tatusov R.L., Soucette-steamm L., Soucallle P., Daly M.J.,

RA

Tatusov R.L., Soucette-steamm L., Soucallle P., Daly M.J.,

RINTS; PRO0834; PROTEASES2C.

REMINTS; PRO0834; PROTEASES2C.

REMAT; SMO0228; PDZ; I.

REMAT; SMO0228; PDZ; I.

REMAT; SMO0228; PDZ; I.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       MEDLINE-21608551; PubMed-11743194;
MEDLINE-21608551; PubMed-11743194;
MEDLINE-21608551; PubMed-11743194;
MEDLINE-21608551; PubMed-11743194;
MILLO B., Gattung S., Miller N., Blanchard M.,
Qurollo B., Goldman B.S., Cao Y., Askenazi M., Halling C., Mullin L.,
Houmiel K., Gordon J., Vaudin M., Iartchouk O., Epp A., Liu F.,
Houmiel K., Gordon J., Vaudin M., Iartchouk O., Epp A., Liu F.,
Holmael K., Gordon J., Vaudin M., Iartchouk O., Epp A., Liu F.,
Holmael C., Slinger M., Doughty D., Scott C., Lappas C., Markelz B.,
Cielo C., Slater S.;
Genece Squence of the plant pathogen and biotechnology agent
Agrobacterium tumefaciens CSB.";
Science 294:2323-2328(2001).
                                                                                                                                                                                                                                                                                                             Nester E.W.; "The genome of the natural genetic engineer Agrobacterium tumefaciens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Gaps
Chen Y., Paulsen I.T., Elsen J.A., Karp P.D., Bovee D. Sr., Chapman P., Clendenning J., Deatherage G., Gillet W., Grant C., Kutyavin T., Levy R., Li M.-J., McClelland E., Palmieri A., Raymond C., Raymond C., Ruse G., Saenphimmachak C., Wu Z., Romero P., Gordon D. Zhang S., Yoo H., Tao Y., Biddle P., Jung M., Krespan W., Perry M., Gordon-Kamm B., Liao L., Kim S., Hendrick C., Zhao Z.-Y., Dolan M., Chumley F., Tingey S.V., Tomb J.-F., Gordon M.P., Olson M.V.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Bacteria; Firmicutes; Bacillus/Clostridium group; Clostridia; Clostridiales; Clostridiales; Clostridium. NCBI_TaxID=1488;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          4.4%; Score 17; DB 16; Length 495; 100.0%; Pred. No. 2.4e-09; Live 0; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Protease; Complete proteome.
SEQUENCE 495 AA; 52681 MW; 36B3887F948F9665 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               01-0CT-2001 (TrEMBLrel. 18, Created)
01-0CT-2001 (TrEMBLrel. 18, Last sequence update)
01-MAR-2002 (TrEMBLrel. 20, Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Serine protease Do (heat-shock protein).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       EMBL; AE009145; AAL42911.1; ALT_INIT.
EMBL; AE008110; AAK87675.1; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                              Science 294:2317-2323(2001).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Clostridium acetobutylicum.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              230 FIQTDASINPGNSGGAL 246
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            121 FIQTDASINPGNSGGAL 137
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Best Local Similarity 100.
Matches 17; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          PRELIMINARY;
```

```
MEDLINE-97000351; PubMed-8843436;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Staphylococcus
                                                                                                                                                                                     Hopwood D.A.;
                                                                                                                                                                                                                                                                                                                       Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        aureus.
                                                                                                                                                                                                                                                                                                                                                                                                                                         099TD6
                                                                                                                                                                                                                                                                                                                                                                                                                   RESULT 12
Q99TD6
                                                                                                                                                                                                                                                                                                                                                                                    g
  ð
                                                                                                                                                                                                                                                                                                                                                                                                                                                    ö
                                                                                                                                                                                                                                                                                                                                                                                                                                         ő
                                                                                                                                                                                                                                  Bacteria; Firmicutes; Bacillus/Clostridium group; Clostridia; Thermoanaerobacteriales; Thermoanaerobacteriace; Thermoanaerobacter. NCBL_TaxID=119072;
                                            Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                         Gaps
                                                                                                                                                                                                                                                                                 SEQUENCE FROM N.A.

STRAIN-MB4T / JCM11007;

MEDLINE-2192816; PubMed=11997336;

Bao Q., Tian Y. Li W., Xu Z., Xuan Z., Hu S., Dong W., Yang J., Chen Y., Xue Y., Xu Y., Lai X., Huang L., Dong X., Ma Y., Ling L., Tan H., Chen R., Wang J., Yu J., Yang H.;

"A complete sequence of T. tengcongensis genome.";

Genome Res. 12:689-700(2002).

EMBL, AE013208; AAM25802.1; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Actinomycetales; Streptomycineae; Streptomycetaceae; Streptomyces.
                                           ö
                                                                                                                                                                                                                                                                                                                                                                                                                                         ;
0
                                                                                                                                                             01-JUN-2002 (TrEMBLrel. 21, Created)
01-JUN-2002 (TrEMBLrel. 21, Last sequence update)
01-JUN-2002 (TrEMBLrel. 21, Last annotation update)
Trypsin-like serine protease, typically periplasmic, contain
                                                                                                                                                                                                                                                                                                                                                                                                                   Length 367;
                      Length 348;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Bentley S.D., Parkhill J., Barrell B.G., Rajandream M.A.;
Submitted (JUL-2001) to the EMBL/GenBank/DDBJ databases.
                    Query Match 3.6%; Score 14; DB 16; Length 34 Best Local Similarity 100.0%; Pred. No. 3.3e-06; Matches 0; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                 3.6%; Score 14; DB 16; Length 36
100.0%; Pred. No. 3.5e-06;
tive 0; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Collins M., Harris D.;
Submitted (JUL-2001) to the EMBL/GenBank/DDBJ databases
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Streptomyces coelicolor.
Bacteria; Firmicutes; Actinobacteria; Actinobacteridae;
36310 MW; 1485D7E9D6FDB2F3 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                  Protease, Complete proteome.
SEQUENCE 367 AA: 39991 MW; A99CB36C029E1AF2 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Last sequence update)
Last annotation update)
                                                                                                                                          367 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        519 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            01-DEC-2001 (TrEMBLrel. 19, Created)
01-DEC-2001 (TrEMBLrel. 19, Last sequ
01-JUN-2002 (TrEMBLrel. 21, Last anno
                                                                                                                                           PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        PRT;
                                                                                                                                                                                                                             Thermoanaerobacter tengcongensis.
                                                                                                                                                                                                                                                                                                                                                                                                                                        14; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        PRELIMINARY;
                                                                                                                                          PRELIMINARY;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Putative protease.
SC03977 OR SCBAC25E3.14.
                                                                122 IQTDASINPGNSGG 135
                                                                           194 IQTDASINPGNSGG 207
                                                                                                                                                                                                                                                                                                                                                                                                                                                            122 IQTDASINPGNSGG 135
                                                                                                                                                                                                                                                                                                                                                                                                                                                                          212 IQTDASINPGNSGG 225
                                                                                                                                                                                                         C-terminal PDZ domain.
DEGQ3 OR TTE2683.
                                                                                                                                                                                                                                                                                                                                                                                                                             Best Local Similarity
Matches 14; Conserve
348 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  NCBI_TaxID-1902;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      STRAIN=A3(2);
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               STRAIN-A3(2);
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            STRAIN-A3(2);
 SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                   Query Match
                                                                                                                                                      Q8R6V1;
                                                                                                                                        Q8R6V1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       093J30
                                                                                                                    RESULT 10
Q8R6V1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                RESULT 11
Q93J30
                                                                                                                                                                                                                                                                                                                                                                                                                                                              δ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                QQ
                                                                ò
                                                                                    윱
```

```
SPECIES=S.aureus (strain Mu50), and S.aureus (strain N315);
MEDLINE=21311952; Pubbed=11418146;
Kuroda M., Ohta F., Uchiyama I., Baba T., Yuzawa H., Kobayashi I.,
Cui L., Oguchi A., Aoki K.-I., Nagai Y., Lian J.-O., Ito T.,
Kanamori M., Matumaru H., Maruyama A., Murakami H., Hosoyama A.,
Mizutani-Ui Y., Yakahashi N.K., Sawano T., Inoue R.-I., Kaito C.,
Sekimizu K., Hirikawa H., Kuhara S., Goto S., Yabuzaki J.,
Kanehisa M., Yamushita A., Oshima K., Furuya K., Yoshino C., Shiba T.,
Hattori M., Ogasuwara N., Hayashi H., Hiramatsu K.,
"Whole genome sequencing of meticillin-resistant Staphylococcus
Redenbach M., Kieser H.M., Denapaite D., Eichner A., Cullum J., Kinashi H., Hopword D.A.;
"A set of ordered cosmids and a detailed genetic and physical map for the 8 Mb Streptomyces coelicolor A3(2) chromosome.";
Mol. Microbiol. 21:77-96(1996).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Gaps
                                                                                                                                                                                     [4]
SECUENCE FROM N.A.
STRAIN-A3(2) / M145;
Bentley S.D., Chatter K.F., Cerdeno-Tarraga A.-M., Challis G.L.,
Thomson N.R., James K.D., Harris D.E., Quail M.A., Kieser H.,
Harper D., Bateman A., Brown S., Chandra G., Chen C.W., Collins M.,
Cronin A., Fraser A., Goble A., Hidalgo J., Hornsby T., Howarth S.,
Hunng C.-H., Kieser T., Larke L., Murphy L., Oliver K., O'Neil S.,
Rabbinowitsch E., Rajandream M.A., Rutherford K., Rutter S.,
Seeger K., Saunders D., Sharp S., Squares R., Squares S., Taylor K.,
Warren T., Wietzoxrek A., Woodward J., Barrell B.G., Parkhill J.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              "Complete genome sequence of the model actinomycete Streptomyces coelicolor A3(2).";
Nature 417:141-147:2002).
EMBL; AL596251; CAC44701.1; -.
InterPro; IPR001478; PDZ.
InterPro; IPR00154; Ser_protease_Try.
Pfam; PF00595; trypsin; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Stabhylococcus aureus (strain Mu50 / ATCC 700699), and Staphylococcus aureus (strain N315).
Bacteria; Firmicutes; Bacillus/Clostridium group; Bacillales;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Length 519;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Hydrolase, Protease, Serine protease.
SEQUENCE 519 AA: 50327 MW; 5CB8D5F0CC19E428 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Lancet 357:1225-1240(2001).
-- SIMILARITY: "O SERINE FOTEASES, TRYPSIN FAMILY.
-- EMBL, APO03363; 3AB57890.1; --
EMBL; APO03134; 3AB42817.1; --
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               01-JUN-2001 (TrEWBLrel. 17, Created)
01-JUN-2001 (TrEWBLrel. 17, Last sequence update)
01-JUN-2002 (TrEWBLrel. 21, Last annotation update)
Hypothetical protein SAV1728.
SAV1728 OR SA1549.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        3.4%; Score 13; DB 16; I
100.0%; Pred. No. 6.1e-05;
Live 0; Mismatches 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  MEROPS, SOL.273; -.
InterPro; IPR001478; PDZ.
InterPro; IPR001940; Protease2C.
InterPro; IPR001254; Ser_protease_Try.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     NCBI_TaxID=158878, 158879;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Best Local Similarity 100.
Matches 13; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   PRELIMINARY;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            123 QTDASINPGNSGG 135
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      352 QTDASINPGNSGG 364
```

RESULT 13 068197 ID 0

g

ò

```
MEDLINE-96239021; PubMed-8675311;
L1 S.R., Dorrell W., Everest P.H., Dougan G., Wren B.W.;
L1 S.R., Dorrell W., Everest P.H., Dougan G., Wren B.W.;
L2 Construction and characterisation of a Yersinia enterocolitica 0:8
L10-60-L-minun. 64:2088-2094 (1996).
L10-60-L-minun. 64:2088-2094 (1996).
HSSP; P29476; LQAV.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Bacteria; Proteobacteria; alpha subdivision; Rhizobiaceae group;
Brucellaceae; Brucella.
     Bacteria; Proteobacteria; gamma subdivision; Enterobacteriaceae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Length 464;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Length 474;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      InterPro; 1PR001478; PDZ.
InterPro; 1PR001940; Protease2C.
InterPro; 1PR0019540; Protease2C.
InterPro; 1PR001954; Ser_protease_Try.
Fram; Pr00595; PDZ; 2.
Pfam; Pr000595; PDZ; 2.
PROTES; PR00834; PROTEASES2C.
SNART; SM00228; PDZ; 2.
PROSITE; PS50106; PDZ; 2.
PROSITE; PS50406; TRYPSTN_DOM: 1.
Hydrolase; Serine protease.
SEQUENCE 474 AA; 50159 MW; F74AC9960C4EF9FB CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         464 AA; 48209 MW; E5D96BF90CFD6542 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               DB 2; Lens
1. 0.00068;
0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               01-NOV-1996 (TrEMBLrel. 01, Created)
01-NOV-1996 (TrEMBLrel. 01, Last sequence update)
01-MAR-2002 (TrEMBLrel. 20, Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          DB 2;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           / Match 3.1%; Score 12; DB Local Similarity 100.0%; Pred. No. 0.(nes 12; Conservative 0; Mismatches
                                                                                                                                                                                                                                                                   InterPro; IPR001478; PDZ.
InterPro; IPR001940; Protease2C.
InterPro; IPR001264; Ser_protease_Try.
InterPro; IPR001265; Ser_proteas_V8.
Pfam; PF00089; trypsin; 1.
PRINTS; PR00839; V8PROTEASES.C.
PRINTS; PR00839; V8PROTEASE.
SMART; SM00228; PDZ; 2.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Score 12;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             MEDLINE-95165990; PubMed-7861951;
                                                                                                                                                                                                                                                                                                                                                                                                                                            PROSITE; PS50106; PDZ; 2.
PROSITE; PS50240; TRYPSIN_DOM; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            3.1%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Hydrolase; Serine protease.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           PRELIMINARY;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          160 GIGFAIPSNMVK 171
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            248 GIGFAIPSNMVK 259
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      HtrA-like protein.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       SEQUENCE FROM N.A.
                                                                               SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Brucella abortus.
                                                                                                                                                                                                                                                     MEROPS; S01.274;
                                         NCBI_TaxID=630;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  NCBI_TaxID=235;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           STRAIN-2308
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       NON_TER
SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         044596
044596;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Matches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     RESULT 15
Q44596
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            g
       ò
                                                                                                                                                                                                ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ö
                                                                                                                                                                                                Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Gaps
Pfam; PF00089; trypsin; 1.
Pfam; PF00089; trypsin; 1.
PROTEASES2C.
SWART; SW00228; PDZ; 1.
PROSTES: PS50240; TRYPSIN_DOW; 1.
Hydrolase; Serine protease; Hypothetical protein; Complete proteome.
SEQUENCE 424 AA; 45803 MW; 888ADBA9A6E97948 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          "The Haemophilus influenzae HtrA protein is a protective antigen.";
Infect. Immun. 66:899-906(1998).
EMBL; AF018151; AAC38202.1; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            MEDLINE-98147697; PubMed-9488373;
Loosmore S.M., Yang Y.P., Comen R., Shortreed J.M., Coleman D.C.,
Klein M.H.;
                                                                                                                                                                                                ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ;
0
                                                                                                                                                                                                                                                                                                                                                                                                                                                              Haemophilus influenzae.
Bacteria: Proteobacteria: gamma subdivision; Pasteurellaceae;
Haemophilus.
                                                                                                                                                          Length 424;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           3.1%; Score 12; DB 2; Length 437; 100.0%; Pred. No. 0.00064; ive 0; Mismatches 0; Indels
                                                                                                                                                                                                0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     SEQUENCE 437 AA; 46376 MW; 27AE2E9F27BE5F6C CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                    01-AUG-1998 (TrEMBLrel. 07, Created)
01-AUG-1998 (TrEMBLrel. 07, Last sequence update)
01-MAR-2002 (TrEMBLrel. 20, Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Q56885 PRELIMINARY; PRT; 464 AA. Q56885; CTEMBLrel. 01, Created) 01-NOV-1996 (TrEMBLrel. 01, Last sequence update) 01-NOV-2002 (TrEMBLrel. 21, Last annotation update)
                                                                                                                                                      Query Match 3.1%; Score 12; DB 16; 18est Local Similarity 100.0%; Pred. No. 0.00062; Matches 12; Conservative 0; Mismatches 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             MEROPS; SO1.274; --
InterPro; IPR001314; Chymotrypsin.
InterPro; IPR001314; Chymotrypsin.
InterPro; IPR001349; PD2.
InterPro; IPR001254; Ser_protease_Try.
Pfam; PF00699; PD2; 2,
Pfam; PR00725; CHYMOTRYPSIN.
PRINTS; PR00722; CHYMOTRYPSIN.
PRINTS; PR00634; PROTEASES_C.
SMART; SM00228; PD2; 2,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          PROSITE; PS50106; PDZ; 2.
PROSITE; PS50240; TRYPSIN_DOM; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Hydrolase; Serine protease.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Query Match 3.1
Best Local Similarity 100.
Matches 12; Conservative
                                                                                                                                                                                                                                                                                                                                                                  PRELIMINARY;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    HtrA protein (Fragment).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Yersinia enterocolitica
                                                                                                                                                                                                                                                       138 YIVTNNHVIDGA 149
                                                                                                                                                                                                                                  22 YIVTNNHVIDGA 33
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      25 TNNHVIDGADKI 36
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          HIHIHIHIH
88 TNNHVIDGADKI 99
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               [1]
SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         NCBI_TaxID=727;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  STRAIN-NTHI 12;
                                                                                                                                                                                                                                                                                                                                                                                      068197;
                                                                                                                                                                                                                                                                                                                                                                  068197
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 RESULT 14
056885
ID 05688
AC 05688
DT 01-NO
DT 01-NO
DT HTRA.
GN HTRA.
```

δ q

ö

Gaps

°; 0; Gaps Best Local Similarity 100.0%; Pred. No. 0.00069; Matches 12; Conservative 0; Mismatches 0; Indels

Qy QQ

Search completed: November 18, 2002, 11:35:08 Job time : 37 secs

```
November 18, 2002, 11:27:10 ; Search time 35 Seconds (without alignments) 2278.292 Million cell updates/sec
                                                                                                                                  US-09-895-913A-120
1938
1 MIPKERMERALGSGVIISKD.......RPKRFLVLDLNQGYRIILVK 387
                                                                                                                                                                                                                                                               671580
GenCore version 5.1.3 Copyright (c) 1993 - 2002 Compugen Ltd.
                                                                                                                                                                                                                                                          Total number of hits satisfying chosen parameters:
                                                                                                                                                                                                                                  671580 seqs, 206047115 residues
                                                                                                                                                                                                                                                                                                                               Post-processing: Minimum Match 0% ... Maximum Match 100% Listing first 45 summaries
                                                      OM protein - protein search, using sw model
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        p_organelle:*
sp_phage:*
sp_phant:*
sp_rodent:*
sp_vrius:*
sp_vurclebrate:*
sp_unclassified:*
sp_rvirus:*
sp_rvirus:*
sp_archeap:*
                                                                                                                                                                                          BLOSUM62
Gapop 10.0 , Gapext 0.5
                                                                                                                                                                                                                                                                                                                                                                                    SPTREMBL_21:*

1: sp_archea:*
2: sp_bacteria:*
3: sp_fungi:*
4: sp_human:*
5: sp_nwertebrate:*
6: sp_mammal:*
                                                                                                                                                                                                                                                                                       Minimum DB seq length: 0 Maximum DB seq length: 2000000000
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     sp_mhc:*
                                                                                                                                                                                                                                                                                                                                                                                                                                             Title:
Perfect score:
Sequence:
                                                                                                                                                                                           Scoring table:
                                                                                                                                                                                                                                                                                                                                                                                     Database :
                                                                                                                                                                                                                                   Searched:
                                                                                Run on:
```

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Description	025663 helicobacte	Q9zm18 helicobacte	Q9pn69 campylobact	046120 campylobact	Q46094 campylobact	Q9kuf5 vibrio chol	Q9fd11 aeromonas h	Q8z9b0 salmonella	067436 aquifex aeo	Q8yh14 brucella me	Q9als1 pseudomonas	Q57155 pseudomonas	Q8rss1 klebsiella	Q9lbk0 shiqella so	044596 brucella ab	Q8zb58 yersinia pe
ΩI	6 025663	6 Q9ZM18	6 Q9PN69	046120	Q46094	6 Q9KUF5	Q9FD11	6 Q8Z9B0	6 067436	6 Q8YHL4	Q9ALS1	6 Q57155	Q8RSS1	Q9LBK0	044596	6 Q8ZB58
Query Match Length DB	443 1	476 1	472 1	472 2	368 2	456 1	453 2	475 1	453 1	474 1	474 2	474 1	477 2	491 2	474 2	457 1
Query Match	100.0	98.8	48.3	48.2	47.5	39.6	38.9	37.0	36.6	36.5	36.5	36.5	36.5	36.4	36.3	36.0
Score	1938	1914	937	934.5	921	767	753.5	717.5	710	707.5	706.5	706.5	706.5	704.5	703.5	869
Result No.	1	~	ĸ	4	ß	9	7	80	σ	10	11	12	13	14	15	16

693.5 35.8 513 16 098CSB 692.5 35.7 523 16 080GQB 6691.5 35.7 403 16 080GQB 675.5 34.9 481 2 09AQD1 667.5 34.4 481 16 082BM 666 34.4 463 2 06B198 667.5 33.4 481 16 092BM 665 33.4 463 2 06B198 652 33.6 455 16 092BM 652 33.6 455 16 092BM 651 33.6 51 33.6 51 4 16 09BM 62 06B1 635.5 32.8 481 16 09BM 62 06B1 635.5 32.8 481 16 09BM 62 06B1 635.5 32.8 481 16 09BM 71 62 06B1 62 0	098cs8 rhizobium 1 08ugg8 agrobacteri 08xy99 ralstronia s 08yg32 brucella me 09agd1 pseudomonas 068197 haemophilus P74978 yersinia en 082bm6 yersinia en 082bm6 yersinia en 080198 haemophilus 09cm3 pasteurella 09cm3 rylella fas 08x36 salmonella 09cm3 xylella fas 08x4f1 escherichia 09cm3 xylella fas 08x5f1 escherichia 08clq1 salmonella 09clq1 xylella fas 08clq1 xylella fas	Q9kjn6 myxococcus Q926c8 rhizobium m
9 9 9 9 9 9 9 9 9 9 9 9 9 9 9 9 9 9 9		2 16
	80000000000000000000000000000000000000	31.2

ALIGNMENTS

us-09-895-913a-120_2.rspt

```
Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Q9PN69;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        09PN69
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          241
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           361
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   RESULT 3
        DR DR DR SO SO
                                                                                                                                                                                                                   à
                                                                                                                                                                                                                                                            g
                                                                                                                                                                                                                                                                                                      ò
                                                                                                                                                                                                                                                                                                                                           셤
                                                                                                                                                                                                                                                                                                                                                                                      à
                                                                                                                                                                                                                                                                                                                                                                                                                             q
                                                                                                                                                                                                                                                                                                                                                                                                                                                                       à
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              요
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ò
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               8
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ò
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    g
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  g
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             DDT THE PROPERTY OF THE PROPER
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             à
                                                                                                                                                                                             ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             240
                                                                                                                                                                                                                                                          AVIRITKDNLPTIKFSDSNDISVGDLVFAIGNPFGVGESVTQGIVSALNKSGIGINSYEN 120
                                                                                                                                                                                                                                                                                                                                           121 FIQTDASINPGNSGGALIDSRGGLVGINTAIISKTGGNHGIGFAIPSNMVKDTVTQLIKT 180
                                                                                                                                                                                                                                                                                                                                                                                                                                                 236
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              137 GKIERGYLGVGLQDLSGDLQNSYDNKEGAVVISVEKDSPAKKAGILVWDLITEVNGKKVK 296
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           300
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 QVEDLTQETKRSMRLSDDVQGVLVSQVNENSPAEQAGFRQGNIITKIEEVEVKSVADFNH 360
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    MEDLINE-99120557; Pubmed-9923682; Alm R.A., Ling L.C., Brown E.D., Doig P.C., Alm R.A., Ling L.-S.L., Moir D.T., King B.L., Brown E.D., Doig P.C., Smith D.R., Noonan B., Gulld B.C., deJonge B.L., Carmel G., Tummino P.J., Caruso A., Uria-Nickelsen M., Mills D.M., Ives C., Gibson R., Merberg D., Mills S.D., Jiang Q., Taylor D.E., Vovis G.F.,
                                                                                                                                                                                               Gaps
                                                                                                                                                                                                                                      9
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        {\tt Irust} \ {\tt I.J.}; "Genomic sequence comparison of two unrelated isolates of the human
                                                                                                                                                                                                                                                                                                                                                                                                                           1 MIPKERMERALGSGVIISKDGYIVTNNHVIDGADKIKVTIPGSNKEYSATLVGTDSESDL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        181 GKIERGYLGVGLQDLSGDLQNSYDNKEGAVVISVEKDSPAKKAGILVWDLITEVNGKKVK
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Helicobacter pylori J99 (Campylobacter pylori J99).
Bacteria; Proteobacteria; epsilon subdivision; Helicobacter group;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         NTNELRNLIGSMLPNORVTLKVIRDKKERAFTLTLAERKNPNKKETISAQNGAQGQLNGL
                                                                                                                                                                                             ó
                                                                                                                                                      Length 443;
SMART; SM00228; PDZ; 2.
PROSITE; PS50106; PDZ; 2.
PROSITE; PS50240; TRYPSIN_DOM; 1.
Hydrolase; Hypothetical protein; Protease; Serine protease;
                                                                                                                                                                                             Indels
                                                                                                        443 AA; 47983 MW; 03FDDBD72CF31EE2 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             gastric pathogen Helicobacter pylori.";
Nature 397:176-180(1999)
-i- SIMILARITY: TO SERINE PROTEASES, TRYPSIN FAMILY.
EMBL: AE001474; AAD05980.1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Last sequence update)
Last annotation update)
                                                                                                                                               100.0%; Score 1938; DB 16;
100.0%; Pred. No. 1.3e-98;
tive 0; Mismatches 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            476 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             MEROPS; S01.273; -.
InterPro; IPR001478; PD2.
InterPro; IPR001940; Protease2C.
InterPro; IPR001254; Ser_protease_Try.
Pfam; PF00595; PD2; 1.
Pfam; PF00089; trypsin; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      443
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          361 ALEKYKGKPKRFLVLDLNQGYRIILVK 387
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Created)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  PRINTS; PR00834; PROTEASES2C
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               01-MAY-1999 (TrEMBLrel. 10, 01-MAY-1999 (TrEMBLrel. 10, 01-JUN-2002 (TrEMBLrel. 21,
                                                                                                                                                                                           Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          PRELIMINARY;
                                                                                                                                                                       Similarity
                                                                                    Complete proteome.
SEQUENCE 443 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  NCBI_TaxID=85963;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    HTRA OR JHP0405.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Helicobacter
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Protease DO
                                                                                                                                                                                         387;
                                                                                                                                                 Query Match
                                                                                                                                                                         Local
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Q92M18
                                                                                                                                                                                           Matches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         241
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  297
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   417
                                                                                                                                                                                                                                                                                                                     61
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         301
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                RESULT 2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      092M18
  SXXDR
                                                                                                                                                                                                                                                                         g
                                                                                                                                                                                                                                                                                                                     ò
                                                                                                                                                                                                                                                                                                                                                          g
                                                                                                                                                                                                                                                                                                                                                                                                                                             셤
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               g
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              g
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 g
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ò
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 g
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            à
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ò
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ò
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       à
```

```
90 MIPKERMERALGSGVIISKDGYIVTNNHVIDGADKIKVTIPGSNKEYSATLVGTDSESDL 149
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   61 AVIRITKDNLPTIKFSDSNDISVGDLVFAIGNPFGVGESVTQGIVSALNKSGIGINSYEN 120
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       NTNELRNLIGSMLPNQRVTLKVIRDKKERAFTLTLAERKNPNKKETISAQNGAQGQLNGL 300
                                                                                                                                                                                                                   Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Parkin-KCTC 11168;
MEDLINE-2015912; PubMed-10688204;
MEDLINE-20159912; PubMed-10688204;
MEDLINE-20159912; PubMed-10688204;
MEDLINE-20159912; PubMed-10688204;
Manaham D., Chillingworth T., Davies R.M., Feltwell T., Holroyd S., Jagels K., Karlyshev A.V., Moule S., Pallen M.J., Penn C.W., Quail M.A., Rajandream M.A., Rutherford K.M., van Vliet A.H.M., Whitehead S., Barrell B.G., "The genome sequence of the food-borne pathogen Campylobacter jejunitereal hypervariable sequences.";
                                                                                                                                                                                                                                                                        1 MIPKERMERALGSGVIISKDGYIVTNNHVIDGADKIKVTIPGSNKEYSATLVGTDSESDL 60
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Campylobacter jejuni.
Bacteria; Proteobacteria; epsilon subdivision; Campylobacter group;
                                                                                                                                                                                                                                                                                                                                                                                                              270 GKIERGYLGVGLQDLSGDLQNSYDNKEGAVVISVEKDSPAKKAGILVWDLITEVNGKKVK
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              181 GKIERGYLGVGLQDLSGDLQNSYDNKEGAVVISVEKDSPAKKAGILVWDLITEVNGKKVK
                                                                                                                                                                                                                   ;
0
                                                                                                                                                           Length 476;
                                                                                                                                                                                                                   Indels
                                                                                Hydrolase; Serine protease; Complete proteome. SEQUENCE 476 AA; 51713 MW; 4E338AED839BFE18 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           01-OCT-2000 (TrEMBLrel. 15, Created)
01-OCT-2000 (TrEMBLrel. 15, Last sequence update)
01-MAR-2002 (TrEMBLrel. 20, Last annotation update)
Serine protease (protease DO) (EC 3.4.21.).
HTRA OR CJ1228C.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   TRYPSIN FAMILY
                                                                                                                                                              98.8%; Score 1914; DB 16; 98.7%; Pred. No. 2.9e-97;
                                                                                                                                                                                                                   1; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            472
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           InterPro; IPR001478; PDZ.
InterPro; IPR001940; Protease2C.
InterPro; IPR001254; Ser_protease_Try.
Pfam; PF00595; PDZ; 2.
Pfam; PF00089; trypsin; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Nature 403:665-668(2000).
-!- SIMILARITY: TO SERINE PROTEASES,
EMBL; AL139077; CAB73482.1; -.
MEROPS; S01.273; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          476
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ALEKYKGKPKRFLVLDLNQGYRIILVK 387
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            PRT;
SMART; SM00228; PD2; 2.
PROSITE; PS50106; PD2; 2.
PROSITE; PS50240; TRYPSIN_DOM; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   450 ALEKYKGKPKRFLVLDLNQGYRIILVK
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    PRINTS; PR00834; PROTEASES2C
                                                                                                                                                                                       Best Local Similarity 98.79
Matches 382; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            PRELIMINARY;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  NCBI_TaxID=197;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Campylobacter
```

m

```
5.
                                                                                                                                                                                                                             70 LPTIKFSDSNDISVGDLVFAIGNPFGVGESVTQGIVSALNKSGIGINSYENFIQTDASIN 129
                                                                                                                                                                                                                                                                                            GSMLPNQRVTLKVIRD -- KKERAFTLTLAERKNPNKKETISAQNGAQGQL - NGLQVEDLT 306
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            307 QETKRSMRLSDDVQGVLVSQVNENSPAEQAGFRQGNIITKIEEVEVKSVADFNHALEKYK 366
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              VGLODLSGDLONSYDNKEGAVVISVEKDSPAKKAGILVWDLITEVNGKKVKNTNELRNLI 249
                                                                                                                                                                                                                                                                                                                                                                                                                                                           342 GTLEIGQKISLSYERDGENKQASFILK-GEKENP------KGVQSDLIDGLSLRNLD 391
                                                                                                                                                                                 Gaps
                                                                                                                                                                10 ALGSGVIISKDGYIVTNNHVIDGADKIKVTIPGSNKEYSATLVGTDSESDLAVIRITKDN 69
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Bacteria; Proteobacteria; epsilon subdivision; Campylobacter group; Campylobacter.
                                                                                                                                  14;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Henderson J., Wood A.C., Emery M.J., Wren B.W., Ketley J., "Characterisation of a Campylobacter jejuni high-temperature-requirement A (htrA) isogenic mutant.";
Submitted (Mar-1997) to the EMBL/GenBank/DDBJ databases.
EMBL; X82628; CAA57948.1; --
MEROPS; S01.273; --
                                                                                                  Length 472;
                                                                                                                                  Indels
SMART; SM00228; PDZ; 2.
PROSITE; PS50106; PDZ; 2.
PROSITE; PS50240; TRYPSIN, DOM; 1.
HYDYCOLASE; SETINE PICTESSE; COMPLETE PICTEOME.
SEQUENCE 472 AA; 51006 MW; DCE4B51540E9894B CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       PROSITE; PS50106; PDZ; 1.
PROSITE; PS50240; TRYPSIN_DOM; 1.
Hydrolase; Protease; Serine protease.
SEQUENCE 472 AA; 50941 MW; OC16E381E97424D1 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         01-NOV-1996 (TrEMBLrel. 01, Created)
01-JUL-1997 (TrEMBLrel. 04, Last sequence update)
01-MAR-2002 (TrEMBLrel. 20, Last annotation update)
                                                                                                                 ; Pred. No. 9.4e-44;
69; Mismatches 102;
                                                                                                48.3%; Score 937; DB 16; 51.3%; Pred. No. 9.4e-44;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          472 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Interpro; IPR001478; PDZ.
Interpro; IPR001449; Protease2C.
InterPro; IPR001244; Ser_protease_fry.
Pfam; PF00089; PDZ; 2.
Pfam; PF00089; Irypsin; 1.
PRIWTS; PR00834; PROTEASES2C.
SWART; SW00228; PDZ; 2.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               | : | |: :||
451 NKKEFTKVWVYRNGFATLLV 470
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            GKPKRFLVLDLNQGYRIILV 386
                                                                                                               Best Local Similarity 51.3
Matches 195; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            PRELIMINARY;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Campylobacter jejuni
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Serine protease.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         NCBI_TaxID=197;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         STRAIN-81116;
                                                                                                  Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          046120
                                                                                                                                                                                                                                                              162
                                                                                                                                                                                                                                                                                              130
                                                                                                                                                                                                                                                                                                                            222
                                                                                                                                                                                                                                                                                                                                                             190
                                                                                                                                                                                                                                                                                                                                                                                                                           250
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          367
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          RESULT 4
Q46120
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ID DATE OF THE PROPERTY OF T
   SKBRR
                                                                                                                                                                                                                                                            g
                                                                                                                                                                                                                                                                                                                           g
                                                                                                                                                                                                                                                                                                                                                                                           q
                                                                                                                                                                                                                                                                                                                                                                                                                                                        g
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            δ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            g
                                                                                                                                                                  ð
                                                                                                                                                                                                                               ò
                                                                                                                                                                                                                                                                                                õ
                                                                                                                                                                                                                                                                                                                                                             ò
                                                                                                                                                                                                                                                                                                                                                                                                                             ò
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         õ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       g
```

```
70 LPTIKFSDSNDISVGDLVFAIGNPFGVGESVTQGIVSALNKSGIGINSYENFIQTDASIN 129
                                                                                                                    342 GTLEIGQKISLSYERDGENKQASFILK-GEKENP------KGVQSDLIDGLSLRNLD 391
                                                                                                                                                                                                                                                                                                                  307 QETKRSMRLSDDVQGVLVSQVNENSPAEQAGFRQGNIITKIEEVEVKSVADFNHALEKYK 366
                          Gaps
                                                  69
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Bacieria; Proteobacteria; epsilon subdivision; Campylobacter group;
Campylobacter,
NCBL_TaxID=197;
                                                  10 ALGSGVIISKDGYIVTNNHVIDGADKIKVTIPGSNKEYSATLVGTDSESDLAVIRITKDN
                                                                                                                                                                                                            190 VGLQDLSGDLQNSYDNKEGAVVISVEKDSPAKKAGILVWDLITEVNGKKVKNTNELRNLI
                                                                                                                                                                                                                                                                250 GSMLPNQRVTLKVIRD--KKERAFTLTLAERKNPNKKETISAQNGAQGQL-NGLQVEDLT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Taylor D.E., Hiratsuka K.; "Use of non-radicactive DNB probes for detection of Campylobacter jejuni and Campylobacter coli in stool specimens."; Mol. Cell. Probes 4:261-271(1990).
 Length 472;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Hiratsuka K.;
Submitted (MAY-1995) to the EMBL/GenBank/DDBJ databases.
EMBL; U27271; AAM68943.1; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            368 AA; 39491 MW; CFA14B08EE49EF70 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       01-NOV-1996 (TrEMNLrel. 01, Created)
01-NOV-1996 (TrEMNLrel. 01, Last sequence update)
01-MAR-2002 (TrEMNLrel. 20, Last annotation update)
         .,3e-43;
 DB 2;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Heat shock protein/serine protease (Fragment)
48.2%; Score 934.5;
52.2%; Pred. No. 1.3e
iive 68; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             MEROPS; S01.273; -.
InterPro; IPR001478; PDZ.
InterPro; IPR001478; PDZ.
InterPro; IPR001134; Ser_protease_Try, Pfam; PF00089; PiDz; 2.
Pfam; PR00089; rypsin; 1.
PRINTS; PR00834; PROFEASES2C.
SMART; SM00228; PDZ; 2.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Hydrolase; Protease; Serine protease.
NON_TER 1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                 PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   MEDLINE-90384493; PubMed-2402249;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      PROSITE; PS50106; PDZ; 1.
PROSITE; PS50240; TRYPSIN_DOM; 1.
                           Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                 PRELIMINARY;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    SEQUENCE FROM N.A. 4
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Campylobacter jejuni
             Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             STRAIN=UA580
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      STRAIN-UA580
                                                                                                                                                                                                                                                                                                                                                                      GK 368
                                                                                                                                                                                                                                                                                                                                                                                              452 KK 453
               Best Local Sir
Matches 189;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             SEQUENCE
 Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                              Q46094
                                                                                                                                                                                                                                                                                                                                                                                                                                                                            046094
                                                                                                                                162
                                                                                                                                                                                                                                                                                                                                                                      367
                                                                                                                                                                                                                                                                                                                                                                                                                                       RESULT 5
Q46094
                                                                            a
                                                                                                      ò
                                                                                                                             g
                                                                                                                                                          ò
                                                                                                                                                                                a
                                                                                                                                                                                                            ŏ
                                                                                                                                                                                                                                    g
                                                                                                                                                                                                                                                              ò
                                                                                                                                                                                                                                                                                     g
                                                                                                                                                                                                                                                                                                                  ŏ
                                                                                                                                                                                                                                                                                                                                           g
                                                                                                                                                                                                                                                                                                                                                                     ŏ
                                                                                                                                                                                                                                                                                                                                                                                              d
```

```
Hydrolase;
 SOW
                                                                                                                                   ò
                                                                                                                                                        g
                                                                                                                                                                                à
                                                                                                                                                                                                       d
                                                                                                                                                                                                                                ò
                                                                                                                                                                                                                                                   g
                                                                                                                                                                                                                                                                               ò
                                                                                                                                                                                                                                                                                                    g
                                                                                                                                                                                                                                                                                                                                                   q
                                                                                                                                                                                                                                                                                                                                                                            ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ò
                                   5
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   SEQUENCE FROM N.A.

STRAIN-EL TOR N16961 / SEROTYPE 01;

MEDLINE-20406633; PubMed=10952301;

Heidelberg J.F., Elsen J.A., Nelson W.C., Clayton R.A., Gwinn M.L.,

Dodson R.J., Haft D.H., Hickey E.K., Peterson J.D., Umayam L.A.,

Gill S.R., Nelson K.E., Read T.D., Tettelin H., Richardson D.,

Ermolaeva M.D., Vamathevan J., Bass S., Qin H., Dragoi I., Sellers P.,

McDonald L., Utterback T., Fleischmann R.D., Nierman W.C., White O.,

Salzberg S.L., Smith H.O., Colwell R.R., Mekalanos J.J., Venter J.C.,
                                                                                                                                                    61 ITETNSDDLMEGDVVFALGNPFGVGFSVTSGIISALNKDNIGLNQYENFIQTDASINPGN 120
                                                                                                                                                                                                    193 QDLSGDLQNSYDNKEGAVVISVEKDSPAKKAGILVWDLITEVNGKKVKNTNELRNLIGSM 252
                                                                                                                                                                                                                   253 LPNQRVTLKVIRD--KKERAFTLTLAERKNPNKKETISAQNGAQGQL-NGLQVEDLTQET 309
                                                                                                                                                                                                                                                                                                   310 KRSMRLSDDQQGVLVSQVNENSPAEQAGFRQGNIITKIEEVEVKSVADFNHALEKYKGKP 369
                                                                                                                                                                                                                                                                                                                  291 KDRLQIPKDVNGVLVHSVKEKSKGKNSGFQEGDIIIGVGQSEIKNLKDLEQAL-KQVNKK 349
                                                                                                       73 IKFSDSNDISVGDLVFAIGNPFGVGESVTQGIVSALNKSGIGINSYENFIQTDASINPGN 132
                                  Gaps
                                                                      SGVIISKDGYIVTNNHVIDGADKIKVTIPGSNKEYSATLVGTDSESDLAVIRITKDNLPT 72
                                                                                                                                                                                                                                                                  Vibrio cholerae.
Bacteria; Proteobacteria; gamma subdivision; Vibrionaceae; Vibrio.
NCBL_TaxID-666;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           'DNA sequence of both chromosomes of the cholera pathogen Vibrio
                                   14;
           Length 368;
          ;; Score 921; DB 2; Length 36E;; Pred. No. 5.1e-43;
69; Mismatches 102; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Nature 406:477-483(2000).
-i- SIMILARITY: TO SERINE PROTEASES, TRYPSIN FAMILY.
EMBL; AE004142; AAF93734.1; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Last sequence update)
Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                      456 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         InterPro; IPR001478; PDZ.
InterPro; IPR001940; Protease2C.
InterPro; IPR001954; Ser_protease_Try.
Pfam; PF001955; PDZ; 2.
Pfam; PF001995; PDZ; 2.
Pfam; PF00199; trypsin; 1.
PRINTS; PR0089; trypsin; 1.
PRINTS; PR00819; PR0TEASES2C.
PROSITE; PS50106; PDZ; 2.
PROSITE; PS50106; PDZ; 2.
                                                                                                                                                                                                                                                                                                                                                                                                                                                              Created)
                                                                                                                                                                                                                                                                                                                                                                                                                                      PRT;
          47.5%;
50.9%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                           01-OCT-2000 (TrEMBLrel. 15, 01-OCT-2000 (TrEMBLrel. 15, 01-MAR-2002 (TrEMBLrel. 20,
                                                                                                                                                                                                                                                                                                                                                   370 KRFLVLDLNQGYRIILV 386
                                                                                                                                                                                                                                                                                                                                                                          350 EFTKVCVYRNGFATLLV 366
                      Best Local Similarity 50.9 Matches 192; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                      PRELIMINARY;
                    Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      MEROPS; S01.274;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   VC0566;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Fraser C.M.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Protease DO
          Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       cholerae.
                                                                                                                                                                                                                                                                                                                                                                                                                                               Q9KUF5;
                                                                                                                                                                                                                                                                                                                                                                                                                                      Q9KUF5
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                TIGR;
                                                                                                                                                                                                                                                                                                                                                                                                              RESULT 6
                                                                                                                                                                                                                                                                                                                                                                                                                         Q9KUF5
                                                                               셤
                                                                                                                               g
                                                                                                                                                                           qq
                                                                                                                                                                                                                                                                           g
                                                                                                                                                                                                                                                                                                                        g
                                                                                                                                                                                                                                                                                                                                                                        g
                                                                                                                                                                                                                                                                                                                                                                                                                                                à
                                                                                                                                                      à
                                                                                                                                                                                                    ð
                                                                                                                                                                                                                           셤
                                                                                                                                                                                                                                                   ö
                                                                                                                                                                                                                                                                                                   à
                                                                                                                                                                                                                                                                                                                                                   ð
```

C . . .

```
8
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 6
                                                                                                                                                                                       324 DIFSELRAKVATLGAGKTITLGVLRDGKNQNIDVTLGEQQNAKTK----AESLHQG-LSG 378
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            :: : | :: | | :: | :: | 379 AELSNTTD-----SDPIQGVKVTEVQKGSAAESYQLQKDDIIIGVNKRYKNIAELR 430
                                                                                                                                                                                                                                                                                                                                                     122 IQTDASINPGNSGGALIDSRGGLVGINTAIISKTGGNHGIGFAIPSNMVKDTVTQLIKTG 181
                                                                                                                                                                                                                                                         63 IRITK-DNLPTIKFSDSNDISVGDLVFAIGNPFGVGESVTQGIVSALNKSGIGINSYENF 121
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 30 LQVEDLTQETKRSMRLSDDVQGVLVSQVNENSPAEQAGFRQGNIITKIEEVEVKSVADFN 359
                                                                                                                 22; Gaps
                                                                                                                                                               4 KERMERALGSGVIISKD-GYIVTNNHVIDGADKIKVTIPGSNKEYSATLVGTDSESDLAV 62
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                              182 KIERGYLGVGLQDLSGDLQNS--YDNKEGAVVISVEKDSPAKKAGILVWDLITEVNGKKV
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        240 KNTNELRNLIGSMLPNQRVTLKVIRDKKERAFTLTLAERKNPNKKETISAQNGAQGQLNG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              27;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Lin T.-N., Lin T.-J., Liou C.-M.; "Aexononas hydrophila strain CKH-29 prtSl gene complete cds."; Submitted (AUG-2000) to the EMBL/GenBank/DDBJ databases. EMBL, AF293977; AAG03073.1; -
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Length 453;
                                                                   Length 456;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Bacteria; Proteobacteria; gamma subdivision; Aeromonadaceae;
                                                                                                                 Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Indels
Serine protease; Complete proteome.
456 Aa; 48366 MW; B4D3912BEB7B0AEE CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       SMACH, SHOULE, PS50106; PD2, 2.
PROSITE; PS50106; TRYPSIN_DOM; 1.
Hydrolase; Protease; Serine protease.
SEGUENCE 453 AA; 47828 MW; BD55CE2B844E5148 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Last sequence update)
Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                38.9%; Score 753.5; DB 2;
43.0%; Pred. No. 1e-33;
:1ve 85; Mismatches 108;
                                                                   39.6%; Score 767; DB 16;
43.6%; Pred. No. 1.8e-34;
tive 83; Mismatches 112;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          453 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         MEROPS; SO1.274; ...
InterPrc; IRR01478; PD2.
InterPrc; IRR010140; PD2.
InterPrc; IRR001240; Ser_protease_Try.
Pfam; PF00089; Lrypsin; 1.
PRINTS; PR00894; PROTEASES2C.
SMART; SM00228; PD2; 2.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Created)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             360 HALEKYKGKPKRFLVLDLNQGYRII 384
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      431 AIME----KSPNILALNIQRGERTL 451
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   01-MAR-2001 (TrEMBLrel. 16, 01-MAR-2001 (TrEMBLrel. 16, 01-MAR-2002 (TrEMBLrel. 20, HtrA-like serine protease.
                                                                                           Best Local Similarity 43.6%
Matches 168; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Query Match
Best Local Similarity 43.09
Matches 166; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          PRELIMINARY;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Aeromonas hydrophila
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         NCBI_TaxID=644;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               STRAIN-CKH-29
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Aeromonas.
                          SEQUENCE
                                                                        Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Q9FD11
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    PRTS1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            RESULT 7
Q9FD11
```

S

us-09-895-913a-120_2.rspt

```
172 KNLTAIKLADSDALRVGDYTVAIGNPFGLGETVTSGIVSALGRSGLNVENYENFIQTDAA 231
                                                                                                                                                                                                                         : : | : | : | : | | | | | | | | | | 398 IEGAEMSNKGQD--KGVVVSSVKANSPAAQIGLKKGDVIIGANQQPVKNIAELRKILD-- 453
                                                                                                 68 DNLPTIKFSDSNI)ISVGDLVFAIGNPFGVGESVTQGIVSALNKSGIGINSYENFIQTDAS 127
                                                                                                                                                                                               INPGNSGGALID/SRGGLVGINTAIISKTGGNHGIGFAIPSNMVKDTVTQLIKTGKIERGY 187
  10 ALGSGVII-SKD(;YIVTNNHVIDGADKIKVTIPGSNKEYSATLVGTDSESDLAVIRI-TK 67
                                                                                                                                                                                                                                                                                                                                                                                                                      LGVGLQDLSGDLANS -- YDNKEGAVVISVEKDSPAKKAGILVWDLITEVNGKKVKNTNEL
                                                                                                                                                                                                                                                                                                                                                                                               RNLIGSMLPNQRVTLKVIRDKKERAFTLTLAERKNPNKKETISAQNGAQGQLNGLQVEDL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             306 TQETKRSMRLSDDVQGVLVSQVNENSPAEQAGFRQGNIITKIEEVEVKSVADFNHALEKY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Deckert G., Warren P.V., Gaasterland T., Young W.G., Lenox A.L., Graham D.E., Overbeek R., Snead W.A., Keller M., Aujay M., Huber Beldman R.A., Short J.M., Olson G.J., Swanson R.V.; "The complete genome of the hyperthermophilic bacterium Aquifex aeolicus.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Bacteria; Aquificae; Aquificales; Aquificaceae; Aquifex.
NCBI_TaxID=63363;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Nature 392:353-358(1998).
-!- SIMILARITY: YO SERINE PROTEASES, TRYPSIN FAMILY.
EMBL; AEOO0741: AACO7399.1; -
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     01-AUG-1998 (TrEMBLrel. 07, Created)
01-AUG-1998 (TrEMBLrel. 07, Last sequence update)
01-MAR-2002 (TrEMBLrel. 20, Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           36.6%; Score 710; DB 16;
41.2%; Pred. No. 2.4e-31;
tive 81; Mismatches 126;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              MERCHS; S01.273; --
InterPro; IPR001,178; PD2.
InterPro; IPR001,148; PD2.
InterPro; IPR001,340; Protease_Try.
Pfam; PF00895; PJD2; 2.
Pfam; PF00089; trypsin; 1.
PRINTS; PR00894; PR0FASESCC.
SMART; SM00228; PD2; 2.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                PROSITE; PS50106: PDZ; 2.
PROSITE; PS50240: TRYPSIN_DOM; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               MEDLINE-98196666; PubMed-9537320;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Periplasmic serine protease
HTRA OR AQ_1450.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               366 KGKPKRFLVLDLNQG 380
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             454 -SKPS-VLALNIQRG 466
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          PRELIMINARY;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             [1]
SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Aquifex aeolicus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        STRAIN=VF5;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Matches 163;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     067436
067436;
                                                                                                                                                                                               128
                                                                                                                                                                                                                                                                                                                                                                                            246
                                                                                                                                                                                                                                                                                                                                                                                                                                             352
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               m
                                                                                                                                                                                                                                                                                                188
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       RESULT 9
067436
                                              g
                                                                                              δλ
                                                                                                                                          q
                                                                                                                                                                                             õ
                                                                                                                                                                                                                                           g
                                                                                                                                                                                                                                                                                                δ
                                                                                                                                                                                                                                                                                                                                       q
                                                                                                                                                                                                                                                                                                                                                                                            ò
                                                                                                                                                                                                                                                                                                                                                                                                                                        ద
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           δ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         g
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               δ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             셤
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ò
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          g
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                RA Parkhill J., Dougan G., James K.D., Thomson N.R., Pickard D., Wain J., RA Churcher C., Mungall K.L., Bentley S.D., Holden M.T.G., Sebaihia M., Basham D., Basham D., Brooks K., Chillingworth T., Connerton P., Concroll A., Davis P., Davises R.M., Dowd L., White N., Farrar J., RA Cronin A., Davis P., Davises R.M., Dowd L., White N., Farrar J., Ra Feltwell T., Hamlin N., Haque A., Hien T.T., Holroyd S., Jagels K., Kroph A., Earsen T.S., Leather S., Moule S., O'Gaora P., Parry C., RA Guail M., Rutherford K., Simmonds M., Skelton J., Stevens K., Whitehead S., Barrell B.G.; RA Quail M., Rutherford K., Simmonds M., Skelton J., Stevens R., Mitchead S., Barrell B.G.; R. Complete genome sequence of a multiple drug resistant Salmonella T. Mature 413:448-822(2001).

R. Mature 413:48-822(2001).

R. Mature 413:48-822(2001).

R. Mitchero; IPR001254; Ser_protease_Try.

R. Mitchero; IPR001254; Ser_protease_Try.

R. Mature 413:48-822(2001).

R. Prim: PF00089; trypsin: 1.

R. Prim: PR00894; PR0FESSE2C.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      6
                                                                                                                                                                                               176
                                                                                                                                                                                                                                                                                                234
                                                                                                                                                                                                                                                                                                                  294
                                                                                                                                                                                                                                                                                                                                                                                                                   :|| ::: || | :| |:| |:| |:| || || DGRAIRSFGELRAKIATMGADKQVALGLIRDGKEQTVKVTL--KKADDSEILASALHPA- 374
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           354
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           422
                                                                                                                        Gaps
2 IPKERME----RALGSGVII-SKDGYIVTNNHVIDGADKIKVTIPGSNKEYSATLVGTDS
                       - LEGAKLS-----TTSEPVSGVAVSEIDPRSPAAASGLQKGDVIIGVNRLRINS
                                                                                            ESDLAVIRITKDNLPTIKFSDSNDISVGDLVFAIGNPFGVGESVTQGIVSALNKSGIGIN
                                                                                                                                                                                               SYENFIQIDASINPGNSGGALIDSRGGLVGINTAIISKTGGNHGIGFAIPSNMVKDTVTQ
                                                                                                                                                                                                                                                                                           LIKTGKIERGYLGVGLQDLSGDLQNS--YDNKEGAVVISVEKDSPAKKAGILVWDLITEV
                                                                                                                                                                                                                                                                                                                                                                                            NGKKVKNTNELRNLIGSMLPNQRVTLKVIRDKKERAFTLTLAERKNPNKKETISAQNGAQ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        GQLNGLQVEDLTQETKRSMRLSDDVQGVLVSQVNENSPAEQAGFRQGNIITKIEEVEVKS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Bacteria; Proteobacteria; gamma subdivision; Enterobacteriaceae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      25;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Length 475;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Query Match 37.0%; Score 717.5; DB 16; Length Best Local Similarity 43.2%; Pred. No. 1e-31; Matches 162; Conservative 74; Mismatches 114; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Heat shock; Complete proteome.
SEQUENCE 475 AA; 49288 MW; C0346749453EAE4B CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                01-MAR-2002 (TrEMBLrel. 20, Created)
01-MAR-2002 (TrEMBLrel. 20, Last sequence update)
01-JUN-2002 (TrEMBLrel. 21, Last annotation update)
Protease DO, heat shock protein HtrA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     475 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         355 VADFNHALEKYKGKPKRFLVLDLNQG 380
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    MEDLINE=21534947; PubMed=11677608;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 PROSITE; PS50106; PDZ; 2.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     PRELIMINARY;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Query Match
Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Salmonella typhi
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Salmonella.
NCBI_TaxID=601;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Q829B0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        295
                                                                                              57
                                                                                                                                                                                                                                           198
                                                                                                                                                                                                                                                                                                                                         258
                                                                                                                                                                                                                                                                                                                                                                                          235
                                                                                                                                                                                          117
                                                                                                                                                                                                                                                                                           177
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  RESULT 8
Q829B0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     DDT TO DD
                                              q
                                                                                                                                                                                                                                                                                                                                  qq
                                                                                                                                                                                                                                                                                                                                                                                          ò
                                                                                                                                                                                                                                                                                                                                                                                                                                        a
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ò
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      g
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ò
ò
                                                                                              ö
                                                                                                                                       g
                                                                                                                                                                                             ò
                                                                                                                                                                                                                                        셤
                                                                                                                                                                                                                                                                                         ò
```

. ک

67 PFTRKERSLGSGVIVKYDEDKKVVYILTNAHVVKNGVRILVKL-DRHTEKKGEIVGIDTK 125 Gaps PKERMERALGSGVIISKDG----YIVTNNHVIDGADKIKVTIPGSNKEYSATLVGTDSE 57 56; Indels Hydrolase; Protense; Serine protease; Complete proteome. SEQUENCE 453 AA; 49958 MW; AC414AB39A60A2DB CRC64; Length

```
150 KIEAKQOFPVLALGNSDEVEVGDLVLAIGNPFGVGQTVTSGIVSAQSRTQVGISDFDFFI 209
                                                                                                                                                                           270 RFERPYIGATFQGITPDLAESLGMEKPYGALITAVVKDGPAETAGLKVGDVVLSVQGVRV
                                                                                                                                                                                                                                                                                                                                               300 IQVEDLTQETKRSMRLSDDVQGVLVSQVNENSPAEQAGFRQGNIITKIEEVEVKSVADFN
                                                                                                                                                                                                                                                                                                                                                                              QTDASINPGNSGALIDSRGGLVGINTAIISKTGGNHGIGFAIPSNMVKDTVTQLIK-TG
                                                                          210 QTDAAINPGNSGGALIDMRGRLIGINTAIYSRSGGSVGIGFAIPSNWVRAVVDAALQGST
                                                                                                                                                                                                                                                240 KNTNELRNLIGSMLPNQRVTLKVIRDKKERAFTLTLAERKNPNKKETISAQNGAQGQLNG
                                                                                                                                                                                                                                                                          182 KIERGYLGVGLQDLSGDLQNS--YDNKEGAVVISVEKDSPAKKAGILVWDLITEVNGKKV
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Created)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     01-JUN-2001 (TrEMBLrel. 17, 01-JUN-2001 (TrEMBLrel. 17, 01-MAR-2002 (TrEMBLrel. 20,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Hydrolase; Serine protease.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Best_Local Similarity 42.09
Matches 159; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          PRELIMINARY;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Pseudomonas aeruginosa
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                474 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               448 AVLEAGRG 455
                                                                                                                                                                                                                                                                                                                                                                                                                                                 360 HALEKYKG 367
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        NCBI_TaxID=287;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Q9ALS1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Q9ALS1
                                                123
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              64
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             149
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            184
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         RESULT 11
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Q9ALS1
                                                                                                                                                                                                                                                                                                                                                                                             g
                                                                                                 쉽
                                                                                                                                                                                             g
                                                                                                                                                                                                                                                   ð
                                                                                                                                                                                                                                                                                              엄
                                                                                                                                                                                                                                                                                                                                               ò
                                                                                                                                                                                                                                                                                                                                                                                                                                                 à
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ACCOORDINATION OF THE REPRESENTATION OF THE PROPERTY OF THE PR
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             q
                                                                                                                                                  à
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              셤
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              à
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                õ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      q
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            õ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              SEQUENCE FROM N.A.

SEQUENCE FROM N.A.

SEQUENCE FROM N.A.

STRAIN=16M / ATCC 23456 / BIOTYPE 1;

NEDLINE=200020109; PubMed=1756688;

DelVecchio V.G., Kapatral V., Redkar R.J., Patra G., Mujer C., Los T.,

Loudous N., Anderson I., Bhattacharyya A., Lykidis A., Reznik G.,

I vanova N., Anderson I., Bhattacharyya A., Lykidis A., Reznik G.,

I vanova N., Anderson I., Bhattacharyya A., Lykidis A., Reznik G.,

Ablonski L., Larsen N., D'Souza M., Bernal A., Mazur M., Goltsman E.,

Selkov E., Elzer P.H., Hagius S., O'Callaghan D., Letesson J.-J.,

Haselkorn R., Kyrpides N., Overbeek R.;

The genome sequence of the facultative intracellular pathogen

Britch and Literals.",

EMBL; AE009519; AAL51964.1; -.

REMBL; AE009519; AAL51964.1; -.

RITCHPO: IPRO0124; Ser_Protease_Try.

RITCHPO: IPRO01254; Ser_Protease_Try.

Refam; PRO0089; trysin; 1.

REMBL; ROORGS4; PROFEASESZC.

REMBL; SMORG28; PDZ; 2.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        υ,
Έ
                                                                                                                                                  SDLAVIRITKDNLPTI-----KFSDSNDISVGDLVFAIGNPFGVGESVTQGIVSALNKSG 112
                                                113 IGINSYENFIQTDASINPGNSGGALIDSRGGLVGINTAIISKTGGNHGIGFAIPSNMVKD 172
                                                                                                                                                                                                                    173 TVTQLIKTGKIERGYLGVGLQDLSGDLQNSYDNKEGAVVISVEKDSPAKKAGILVWDLIT 232
                                                                                                                                                                                                                                                EVNGKKVKNTNELRNLIGSMLPNQRVTLKVIRDKKERAFTLTLAERKNPNKKETISAQNG 292
                                                                                                                                                                                                                                                                                                                                                  64 RI-TKDNLPTIKFSDSNDISVGDLVFAIGNPFGVGESVTQGIVSALNKSGIGINSYENFI 122
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 4 KERMERALGSGVIISKDGYIVTNNHVIDGADKIKVTIPGSNKEYSATLVGTDSESDLAVI 63
                                                                                                                                                                                                                                                                                                                                                                                                                                                   | : || : || : || | : || | 358 ATPENLGLLLENDLTLKEKQEAGVP---YGVLVEGIYPDSPAEYSGLQPGDIILKVNNRPV
                                                                                                                                                                                                                                                                                                                                                                                                                    293 AQGQLNGLQVEDLTQETKRSMRLSDDVQGVLVSQVNENSPAEQAGFRQGNIITKIEEVEV
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Bacteria; Proteobacteria; alpha subdivision; Rhizobiaceae group;
Brucellaceae; Brucella.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                36.5%; Score 707.5; DB 16; Length 474; llarity 42.1%; Pred. No. 3.5e-31; Conservative 74; Mismatches 132; Indels 7;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    1AFE49860C4EFA14 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Last sequence update)
Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    :|| :| | : : | | : : | | : : 415 RSVREFYEIINRLKEMGRSKALLL--VRRGDRNIFI 448
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      353 KSVADFNHALEKYK--GKPKRFLVLDLNQGYRIILV 386
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               474 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Created)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Hydrolase; Complete proteome.
SEQUENCE 474 AA; 50153 MW;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        01-MAR-2002 (TrEMBLrel. 20
01-MAR-2002 (TrEMBLrel. 20
01-JUN-2002 (TrEMBLrel. 21.
Protease DO (EC 3.4.21.-).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      PROSITE; PS50106; PDZ; 2.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               PRELIMINARY;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Brucella melitensis.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           NCBI_TaxID-29459;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                155;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Local
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Q8YHL4;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Q8YHL4
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Best Loca
Matches
                    58
                                                                                                                                                                                                                                                                                                                      233
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            RESULT 10
                                                                                                                                                                                                                                                                                                                                                                 g
                                                                                                                                                                                                                                                                                                                                                                                                                                                                  g
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      g
                                                                     q
                                                                                                                     ò
                                                                                                                                                                 g
                                                                                                                                                                                                                       à
                                                                                                                                                                                                                                                                  g
                                                                                                                                                                                                                                                                                                                ò
                                                                                                                                                                                                                                                                                                                                                                                                                       ò
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ò
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    9
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ô
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ò
```

```
RITKDNLPTIKFSDSNDISVGDLVFAIGNPFGVGESVTQGIVSALNKSGIGINSYENFIQ 123
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           124 TDASINPGNSGALIDSRGGLVGINTAIISKTGGNHGIGFAIPSNMVKDTVTQLIKTGKI 183
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ERGYLGVGLQDLSGDLQNSY -- DNKEGAVVISVEKDSPAKKAGILVWDLITEVNGKKVKN 241
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             4 KERMERALGSGVIISKDGYIVTNNHVIDGADKIKVTIPGSNKEYSATLVGTDSESDLAVI 63
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Bacteria; Proteobacteria; gamma subdivision; Pseudomonadaceae;
Pseudomonas.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Length 474;
                                                                                                                                                                                                                                                                                                                                                                                 Yorgey P.S., Rahme L.G., Tan M., Ausubel F.M.;
Yorgey P.S., Rahme L.G., Tan M., Ausubel F.M.;
The Roles of muco and Alginate in the Virulence of Pseudom earuginosa in Plants, Nemacodes, and Mice.";
Submitted (JAN-2001) to the EMBL/GenBank/DDBJ databases.
Submitted (JAN-2001) to the EMBL/GenBank/DDBJ databases.
REMBL, ARA13973, AAR11276.1;
InterPro; IPR0014748; Pro.
InterPro; IPR0014748; Pro.
InterPro; IPR0014748; Pro.
InterPro; IPR001545; Ser_Protease_Try.
Pfam: PF00595; Pro.; 2.
Pfam: PF00689; trypsin: 1.
RPINTS; PR00884; PROTEASES2C.
SMART; SMART; SM00228; PDZ; 2.
RPOSITE; PS500240; TRYPSIN_DOM; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 50349 MW; A22FD4338B859D4C CRC64;
                                                                                          Last sequence update)
Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   36.5%; Score 706.5; DB 2;
42.0%; Pred. No. 4e-31;
tive 76; Mismatches 127;
474 AA
```

```
ώ
Έ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   6
                                                                                                                                                                                                                                                                                                           64 RITKDNLPTIKFSDSNDISVGDLVFAIGNPFGVGESVTQGIVSALNKSGIGINSYENFIQ 123
                                                                                                                                                                                                                                                                                                                                                                                                                             124 TDASINPGNSGGALIDSRGGLVGINTAIISKTGGNHGIGFAIPSNMVKDTVTQLIKTGKI 183
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                184 ERGYLGVGLQDL&GDLQNSY--DNKEGAVVISVEKDSPAKKAGILVWDLITEVNGKKVKN 241
                                                                                                                                                                                                                                                          Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Gaps
                                                                                                                                                                                                                                                                                         4 KERMERALGSGVIISKDGYIVTNNHVIDGADKIKVTIPGSNKEYSATLVGTDSESDLAVI 63
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    10 ALGSGVII-SKDGYIVTNNHVIDGADKIKVTIPGSNKEYSATLVGTDSESDLAVIRI-TK 67
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  268 SRGWLGVVIQEVNKDLAESFGLDKPSGALVAQLVEDGPAAKGGLQVGDVILSLNGQSINE
                                                                                                                                                                                                                                                                                                                                                                                SADLPHLYGNWKPGDKINLDVIRNGQRK--SLSMAVGSLPDDDEEIASMGAPGAERSSNR
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   299 -GLQVEDLTQET(REMRLSDDVQGVLVSQVNENSPAEQAGFRQGNIITKIEEVEVKSV--
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                242 THELRNLIGSMLPNORVTLKVIRDKKERAFTLTLAERKNPNKKETISAON--GAQGQLN-
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Klebsiella pneumcniae.
Bacteria; Proteobacteria; gamma subdivision; Enterobacteriaceae;
                                                                                                                                                                                                                                                        17;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   25;
                                                                                                                                                                                                                   36.5%; Score 706.5; DB 16; Length 474; 41.7%; Pred. No. 4e-31; Live 78; Mismatches 126; Indels 17;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Query Match 36.5%; Score 706.5; DB 2; Length 477; Best Local Similarity 42.7%; Pred. No. 4e-31; Matches 160; Conservative 74; Mismatches 116; Indels 25
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           "Role of the htrN gene in Klebsiella pneumoniae virulence.";
Submitted (FEB-2002) to the EMBL/GenBank/DDBJ databases.
EMBL; AJ430233; (AD22887.1; -.
                                                                                                                             PROSITE; PS50240; PD2; 2.
PROSITE; PS50240; IRYPSIN_DOM; 1.
Hydrolase; Protease; Serine protease; Complete proteome.
SEOUENCE 474 AA; 50321 MW; BAB5D2A89867BEBE CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              477 AN; 49559 MW; 28D22FAE59FCF487 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Last sequence update)
Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ¥.
            InterPro; IPR001478; PDZ.
InterPro; IPR001940; Protease2C.
InterPro; IPR001254; Ser_protease_Try.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      01-JUN-2002 (TrEMBLrel. 21, Created)
01-JUN-2002 (TrEMBLrel. 21, Last seq
01-JUN-2002 (TrEMBLrel. 21, Last ann
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          PRT;
EMBL; AE004511; AAG04155.1; -.
                                                                 Pfam; PF00595; PDZ; 2.
Pfam; PF00089; trypsin; 1.
PRINTS; PR00834; PROTEASES2C.
SMART; SM00228; PDZ; 2.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  -ADFNHALEKYKSKPKRFL 373
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         442 FADVAKALPKNRSVSMRVL 460
                                                                                                                                                                                                                      Query Match 36.55
Best Local Similarity 41.77
Matches 158; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          PRELIMINARY;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            NCBI_TaxID=573;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           HtrA protein.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Klebsiella
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Cortes G.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        08RSS1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Q8RSS1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      356
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 328
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        RESULT 13
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Q8RSS.
   ò
                                                                                                                                                                                                                                                                                                                         g
                                                                                                                                                                                                                                                                                                                                                          ò
                                                                                                                                                                                                                                                                                                                                                                                          g
                                                                                                                                                                                                                                                                                                                                                                                                                             ŏ
                                                                                                                                                                                                                                                                                                                                                                                                                                                          g
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ò
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              g
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ŏ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 g
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   'n
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 g
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ò
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  g
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ŏ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           SETAINT-ATC 15692 / PAO1;
MEDLINE-95286510; PubMed-1768826;
WHENLINE-95286510; PubMed-1768826;
Yu H., Schurr M.J., Deretto V.;
"Functional equivalence of Escherichia coli sigma E and Pseudomonas aeruginosa Algui E. Coli rpoE restores mucoidy and reduces sensitivity to reactive oxygen intermediates in algU mutants of P. aeruginosa.;
J. Bacteriol. 177:3259-3268(1995).
299 -GLQVEDLTQETKRSMRLSDDVQGVLVSQVNENSPAEQAGFRQGNIITKIEEVEVKSV-- 355
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Stover C.K., Pham X.-Q.T., Erwin A.L., Mizoguchi S.D., Warrener P., Hickey M.J., Brinkman F.S.L., Hufnagle W.O., Kowalik D.J., Lagrou M., Garber R.L., Goltry L., Tolentino E., Westbrock-Wadman S., Yuan Y., Brody L.L., Coulter S.N., Folger K.R., Kas A., Larbig K., Lim R.M., Smith K.A., Spencer D.H., Wong G.K.-S., Wu Z., Paulsen I.T., Reizer J., Saier M.H., Hancock R.E.W., Lory S., Olson M.V.; "Complete genome sequence of Pseudomonas aeruginosa PAO1, an
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     "Two distinct loci affecting conversion to mucoidy in Pseudomonas aeruginosa in cystic fibrosis encode homologs of the serine protease
                                                                    SADLPHLVGNMKPGDKINLDVIRNGQRK--SLSMAVGNLPDDDEEIASMGAPGAERSSNR
                                                                                                                                     TNELRNLIGSMLPNORVTLKVIRDKKERAFTLTLAERKNPNKKETISAON--GAOGOLN-
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Boucher J.C., Martinez-Salazar J., Schurr M.J., Mudd M.H., Yu H.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Martin D.W., Schurr M.J., Mudd M.H., Govan J.R., Holloway B.W.,
                                                                                                                                                                                                                                                                                                                                                                                                                                           Bacteria; Proteobacteria; gamma subdivision; Pseudomonadaceae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Mechanism of conversion to mucoidy in Pseudomonas aeruginosa
infecting cystic fibrosis patients.";
Proc. Natl. Acad. Sci. U.S.A. 90:8377-8381(1993).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Nature 406:959<sup>+</sup>964(2000).
-- SIMILARITY: TO SERINE PROTEASES, TRYPSIN FAMILY.
EMBL; 049151; AAC47718.1; --
EMBL; U32853; AAC43676.1; --
                                                                                                                                                                                                                                                                                                                                     01-NOV-1996 (TrEMBLrel. 01, Created)
01-NOV-1996 (TrEMBLrel. 01, Last sequence update)
01-JUN-2002 (TrEMBLrel. 21, Last annotation update)
MUCD (Serine protease MUCD).
                                                                                                                                                                                                                                                                                                       474 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      SEQUENCE FROM N.A.
STRAIN-ATCC 15692 / PAO1;
MEDLINE-20437337; PubMed-10984043;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 SEQUENCE FROM N.A.
STRAIN-ATCC 15692 / PAO1;
MEDLINE-96134987; PubMed-8550474;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           SEQUENCE FROM N.A.
STRAIN-ATCC 15692 / PAO1;
MEDLINE-93391358; Pubmed-8378309;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Bacteriol. 178:511-523(1996)
                                                                                                                                                                                     356 -ADFNHALEKYKGKPKRFL 373
                                                                                                                                                                                                                 442 FADVAKALPKNRSVSMRVL 460
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   opportunistic pathogen.";
                                                                                                                                                                                                                                                                                                       PRELIMINARY;
                                                                                                                                                                                                                                                                                                                                                                                                                             Pseudomonas aeruginosa.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                           NCBI_TaxID=287;
                                                                                                                                                                                                                                                                                                                                                                                                          MUCD OR PA0766
                                                                                                                                                                                                                                                                                                                                                                                                                                                               Pseudomonas
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Deretic V.;
                                                                                                                                                                                                                                                                                                      057155
                                                 242
                                                                                                                                                  386
                                                                                                                                                                                                                                                                      RESULT 12
                                                                                                                                                                                                                                                                                        057155
                                                                                                                                                                                                                 g
                                                                                                                                                                                                                                                                                                       à
                                                                               g
                                                                                                                ò
                                                                                                                                                  g
                                                                                                                                                                                     à
```

œ

```
231 INRGNSGGALVNLNGELIGINTAILAPDGGNIGIGFAIPSNMVINLTSQMVEYGQVKRGE 290
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         50159 MW; F74AC9960C4EF9FB CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Last sequence update)
Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Query Match 36.3%; Score 703.5; DB 2; Best Local Similarity 41.8%; Pred. No. 5.8e-31; Matches 154; Conservative 74; Mismatches 133;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                          474 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                MEROPS; S01.273; -...
InterPro; IPR001478; PDZ.
InterPro; IPR001478; PDZ.
InterPro; IPR00140; Protease2C.
InterPro; IPR001254; Ser_protease_Try.
Pfam; PF00089; trypsin; 1.
PRam; PF00089; trypsin; 1.
PRAFTY; SM0028; PDZ; 2.
PROSITE; PS50106; PDZ; 2.
PROSITE; PS50106; PDZ; 2.
PROSITE; PS50240; TRYPSIN_DOM; 1.
Hydrolase; Serine protease.
SEQUENCE 474 AA; S0159 WW; F74AC9960C
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Created)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                          PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    MEDLINE-95165990; PubMed-7861951;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    01-NOV-1996 (TrEMBLrel. 01, 01-NOV-1996 (TrEMBLrel. 01, 01-MAR-2002 (TrEMBLrel. 20,
                                                                                                                                                                                                                                                                                                                   366 KGKPKRFLVLDLNQGYR 382
                                                                                                                                                                                                                                                                                                                                               PRELIMINARY;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Brucellaceae; Brucella.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                NCBI_TaxID=235;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               STRAIN-2308
                                                                                                                                                                                                                                                                         400
                                            188
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 64
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     123
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 210
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        270
                                                                                                                                                                              g
                                                                                                                                                                                                                                                                         g
                                                                                                                                                                                                                                                                                                                                                             셤
                                                                                        음
                                                                                                                                                                                                                             ö
                                                                                                                                                                                                                                                                                                                     ð
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         DDT RELEASE SO DE STANDER SO DE STANDER SE STANDER SE STANDER SE STANDER SO DE STANDER
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     g
                                                                                                                                    ò
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ò
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         g
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       õ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 g
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              à
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     q
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 8;
                                                                                                                                                            115 ALGSGVIIDAAKGYVVTNNHVVDNATTIKVQL-SDGRRFDAKVVGKDPRSDIALIQIQDP 173
                                                                   LGVGLQDLSGDLQNS--YDNKEGAVVISVEKDSPAKKAGILVWDLITEVNGKKVKNTNEL 245
                                                                                                                                                                                                                                                    246 RNLIGSMLPNQRVTLKVIRDKKERAFTLTLAERKNPNKKETISAQNGAQGQLNGLQVEDL 305
                                                                                                                                                                                                                                                                                                                                                                                                         306 TQETKRSMRLSDDVQGVLVSQVNENSPAEQAGFRQGNIITKIEEVEVKSVADFNHALEKY 365
                                                                                                                                                                                                                                                                                                                                                                                                                                68 DNLPTIKESDSNDISVGDLVFAIGNPFGVGESVTQGIVSALNKSGIGINSYENFIQTDAS 127
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      68 DNLPTIKFSDSNDISVGDLVFAIGNPFGVGESVTQGIVSALNKSGIGINSYENFIQTDAS 127
                                                                                                                                  128 INPGNSGGALIDSRGGLVGINTAIISKTGGNHGIGFAIPSNMVKDTVTQLIKTGKIERGY 187
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         10 ALGSGVIISKD-GYIVTNNHVIDGADKIKVTIPGSNKEYSATLVGTDSESDLAVIRI-TK 67
                                                                                                                                                                                                                                                                                                                                          Shigella sonnei.
Bacteria; Proteobacteria; gamma subdivision; Enterobacteriaceae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          complete cds.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 25;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Length 491;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Morita K., Watanabe N., Kanamori M.;
"Shigalla sonnei strain 97-201 HtrA (htrA) gene, complete of submitted (MAR-2000) to the EMBL/GenBank/DDBJ databases.
EMBL; AB040030; BAA92745.1; --
InterPro; IPR001478; PDZ.
InterPro; IPR001478; PDZ.
InterPro; IPR001340; Protease2C.
InterPro; IPR001254; Ser_Protease_Try.
Pfam; PF00595; PDZ; 2.
Pfam; PF00089; trypsin; 1.
PRINTS; PR00894; PROTEASES2C.
SMART; SM00228; PDZ; 2.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         51358 MW; 8E5F6E9F74B0E46B CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Last sequence update)
Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                36.4%; Score 704.5; DB 2; 42.7%; Pred. No. 5.4e-31; ive 71; Mismatches 120;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         491 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Created)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   PROSITE; PS50106; PDZ; 2.
PROSITE; PS50240; TRYPSIN_DOM; 1.
Hydrolase; Serine protease.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              01-0CT-2000 (TrEMBLrel. 15, 01-0CT-2000 (TrEMBLrel. 15, 01-MAR-2002 (TrEMBLrel. 20, Heat shock protein HtrA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Matches 161; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               366 KGKPKRFLVLDLNQG 380
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           || | |:::|
455 DAKPS-VLALNIORG 468
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         PRELIMINARY;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         491 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  NCBI_TaxID=624;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Q9LBK0
Q9LBK0;
                                                                                                                                                                                                                        188
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          RESULT 14
Q9LBK0
                                                                                                                                                                                                                                                                                                                                                           8
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            g
                                                                                        a
                                                                                                                                                                            a
                                                                                                                                                                                                                          ò
                                                                                                                                                                                                                                                                  g
                                                                                                                                                                                                                                                                                                              ò
                                                                                                                                                                                                                                                                                                                                                                                                         ò
                                                                                                                                                                                                                                                                                                                                                                                                                                                 a
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               à
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         g
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ò
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ò
                                            ò
                                                                                                                                à
```

```
246 RNLIGSMLPNQRVTLKVIRDKKERAFTLTLAERKNPNKKETISAQNGAQGQLNGLQVEDL 305
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  RI-TKDNLPTIKFSDSNDISVGDLVFAIGNPFGVGESVTQGIVSALNKSGIGINSYENFI 122
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  QTDASINPGNSGGALIDSRGGLVGINTAIISKTGGNHGIGFAIPSNMVKDTVTQLIK-TG 181
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         KIERGYLGVGLQDLSGDLQNS--YDNKEGAVVISVEKDSPAKKAGILVWDLITEVNGKKV 239
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               4 KERMERALGSGVIISKDGYIVTNNHVIDGADKIKVTIPGSNKEYSATLVGTDSESDLAVI 63
                                                                                                     LGVGLQDLSGDLQNS--YDNKEGAVVISVEKDSPAKKAGILVWDLITEVNGKKVKNTNEL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               306 TQETKRSMRLSDDVQGVLVSQVNENSPAEQAGFRQGNIITKIEEVEVKSVADFNHALEKY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Tatum F.M., Cheville N.F., Morfitt D.; "Cloning, characterization and construction of htrA and htrA-like mitants of Brucella abortus and their survival in BALB/c mice."; Microb. Pathog. 17:23-36(1994).
EMBL; U07351; AAA70163.1; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                     | :|:| ::|| ::|| |: | | :: |: | || :| | |: | | :| | | :| | | :| | | :| | :| | :| | :| | :| | :| | :| | :| | :| | :| | :| | :| | :| | :| | :| | :| | :| | :| | :| | :| | :| | :| | :| | :| | :| | :| | :| | :| | :| | :| | :| | :| | :| | :| | :| | :| | :| | :| | :| | :| | :| | :| | :| | :| | :| | :| | :| | :| | :| | :| | :| | :| | :| | :| | :| | :| | :| | :| | :| | :| | :| | :| | :| | :| | :| | :| | :| | :| | :| | :| | :| | :| | :| | :| | :| | :| | :| | :| | :| | :| | :| | :| | :| | :| | :| | :| | :| | :| | :| | :| | :| | :| | :| | :| | :| | :| | :| | :| | :| | :| | :| | :| | :| | :| | :| | :| | :| | :| | :| | :| | :| | :| | :| | :| | :| | :| | :| | :| | :| | :| | :| | :| | :| | :| | :| | :| | :| | :| | :| | :| | :| | :| | :| | :| | :| | :| | :| | :| | :| | :| | :| | :| | :| | :| | :| | :| | :| | :| | :| | :| | :| | :| | :| | :| | :| | :| | :| | :| | :| | :| | :| | :| | :| | :| | :| | :| | :| | :| | :| | :| | :| | :| | :| | :| | :| | :| | :| | :| | :| | :| | :| | :| | :| | :| | :| | :| | :| | :| | :| | :| | :| | :| | :| | :| | :| | :| | :| | :| | :| | :| | :| | :| | :| | :| | :| | :| | :| | :| | :| | :| | :| | :| | :| | :| | :| | :| | :| | :| | :| | :| | :| | :| | :| | :| | :| | :| | :| | :| | :| | :| | :| | :| | :| | :| | :| | :| | :| | :| | :| | :| | :| | :| | :| | :| | :| | :| | :| | :| | :| | :| | :| | :| | :| | :| | :| | :| | :| | :| | :| | :| | :| | :| | :| | :| | :| | :| | :| | :| | :| | :| | :| | :| | :| | :| | :| | :| | :| | :| | :| | :| | :| | :| | :| | :| | :| | :| | :| | :| | :| | :| | :| | :| | :| | :| | :| | :| | :| | :| | :| | :| | :| | :| | :| | :| | :| | :| | :| | :| | :| | :| | :| | :| | :| | :| | :| | :| | :| | :| | :| | :| | :| | :| | :| | :| | :| | :| | :| | :| | :| | :| | :| | :| | :| | :| | :| | :| | :| | :| | :| | :| | :| | :| | :| | :| | :| | :| | :| | :| | :| | :| | :| | :| | :| | :| | :| | :| | :| | :| | :| | :| | :| | :| | :| | :| | :| | :| | :| | :| | :| | :| | :| | :| | :| | :| | :| | :| | :| | :| | :| | :| | :| | :| | :| | :| | :| | :| | :| | :| | :| | :| | :| | :| | :| | :| | :| | :| 
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                HtrA-like protein.
Brucella abortus.
Bacteria; Proteobacteria; alpha subdivision; Rhizobiaceae group;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               7;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Length 474;
```

., 2

Search completed: November 18, 2002, 11:29:40 Job time: 38 secs

	;·		
		•	
*			
÷ .			
÷)			
<i>'</i>			3
			Ÿ

```
MEDLINE=97000351; PubMed=8843436;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   MEROPS; S01.273; -
                                                                                                                                                                                                                                                                                                                                                       Hopwood D.A.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 099TD6
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         RESULT 12
Q99TD6
    ò
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             g
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ;
0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ó
                                                                                                                                                                                                                                                                                                                                                                                                                                                   Bacteria; Firmicutes; Bacillus/Clostridium group; Clostridia; Thermoanaerobacteriales; Thermoanaerobacteriaceae; Thermoanaerobacter. NCBL_TaxID=119072;
                                                                                   Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               STRAIN-MB4T / JCM11007;
STRAIN-MB4T / JCM11007;
MEDILINE-12992816; PubMed-11997336;
MEDILINE-12992816; PubMed-11997336;
MEDILINE-12992816; PubMed-11997336;
Chen Y., Xue Y., Xu Y., Zu, Xu Z., Xuan Z., Hu S., Dong W., Yang J., Chen Y., Xue Y., Xu Y., Yang L., Dong X., Ma Y., Ling L., Tan H., Chen R., Wang J., Yu J., Yang H.;
"A complete sequence of T. tengcongensis genome.";
Genome Res. 12:689-700(2002).
EMBL; AE013208; AAM25802.1; -.
Protease: Complete proteome.
SEQUENCE 367 AA, 39991 MW; A99CB36C029E1AF2 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Streptomyces coelicolor
Bacteria; Firmicutes; Actinobacteria; Actinobacteridae;
Actinomycetales; Streptomycineae; Streptomyces.
                                                                                 ;
0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 .;
0
                                                                                                                                                                                                                                                                                                        01-JUN-2002 (TrEMBLrel. 21, Created)
01-JUN-2002 (TrEMBLrel. 21, Last sequence update)
01-JUN-2002 (TrEMBLrel. 12, Last annotation update)
Trypsin-like serine protease, typically periplasmic, contain
                                          Length 348;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Length 367;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       STRAIN-A3(2);
Bentley S.D., Parkhill J., Barrell B.G., Rajandream M.A.;
Submitted (JUL-2001) to the EMBL/GenBank/DDBJ databases.
                                                                              Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       STRAIN*A3(2);
Collins M., Harris D.;
Submitted (JUL-2001) to the EMBL/GenBank/DDBJ databases
348 AA; 36310 MW; 1485D7E9D6FDB2F3 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Last sequence update)
Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  3.6%; Score 14; DB 16; I
100.0%; Pred. No. 3.5e-06;
tive 0; Mismatches 0;
                                    3.6%; Score 14; DB 16; I
Local Similarity 100.0%; Pred. No. 3.3e-06;
les 14; Conservative 0; Mismatches 0;
                                                                                                                                                                                                                                                                      A
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Created)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                PRT;
                                                                                                                                                                                                                                                                      PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                    Thermoanaerobacter tengcongensis
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       01-DEC-2001 (TrEMBLrel. 19, 01-DEC-2001 (TrEMBLrel. 19, 01-JUN-2002 (TrEMBLrel. 21,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Putative protease.
SCO3977 OR SCBAC25E3.14.
                                                                                                                                                                                                                                                                    PRELIMINARY;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               14; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  PRELIMINARY;
                                                                                                                       122 IQTDASINPGNSGG 135
                                                                                                                                            194 IQTDASINPGNSGG 207
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      122 IQTDASINPGNSGG 135
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           212 IQTDASINPGNSGG 225
                                                                                                                                                                                                                                                                                                                                                                                             C-terminal PDZ domain.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  [2]
SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                DEGQ3 OR TTE2683.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         NCBI_TaxID=1902;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               STRAIN-A3(2)
  SQ SEQUENCE
                                      Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      093330;
                                                                                                                                                                                                                                                                  08R6V1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                093330
                                                                                                                                                                                                                                                                                       Q8R6V1
                                                                                 Matches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Matches
                                                                                                                                                                                                                             RESULT 10
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            RESULT 11
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         20330

20330

20330

20330

20330

20330

20330

20330

20330

20330

20330

20330

20330

20330

20330

20330

20330

20330

20330

20330

20330

20330

20330

20330

20330

20330

20330

20330

20330

20330

20330

20330

20330

20330

20330

20330

20330

20330

20330

20330

20330

20330

20330

20330

20330

20330

20330

20330

20330

20330

20330

20330

20330

20330

20330

20330

20330

20330

20330

20330

20330

20330

20330

20330

20330

20330

20330

20330

20330

20330

20330

20330

20330

20330

20330

20330

20330

20330

20330

20330

20330

20330

20330

20330

20330

20330

20330

20330

20330

20330

20330

20330

20330

20330

20330

20330

20330

20330

20330

20330

20330

20330

20330

20330

20330

20330

20330

20330

20330

20330

20330

20330

20330

20330

20330

20330

20330

20330

20330

20330

20330

20330

20330

20330

20330

20330

20330

20330

20330

20330

20330

20330

20330

20330

20330

20330

20330

20330

20330

20330

20330

20330

20330

20330

20330

20330

20330

20330

20330

20330

20330

20330

20330

20330

20330

20330

20330

20330

20330

20330

20330

20330

20330

20330

20330

20330

20330

20330

20330

20330

20330

20330

20330

20330

20330

20330

20330

20330

20330

20330

20330

20330

20330

20330

20330

20330

20330

20330

20330

20330

20330

20330

20330

20330

20330

20330

20330

20330

20330

20330

20330

20330

20330

20330

20330

20330

20330

20330

20330

20330

20330

20330

20330

20330

20330

20330

20330

20330

20330

20330

20330

20330

20330

20330

20330

20330

20330

20330

20330

20330

20330

20330

20330

20330

20330

20330

20330

20330

20330

20330

20330

20330

20330

20330

20330

20330

20330

20330

20330

20330

20330

20330

20330

20330

20330

20330

20330

20330

20330

20330

20330

20330

20330

20330

20330

20330

20330

20330

20330

20330

20330

20330

20330

20330

20330

20330

20330

20330

20330

20330

20330

20330

20330

203300

203300

203300

203300

203300

20330

20330

20330

2033
                                                                                                                                                                                                                                              Q8R6V1
                                                                                                                                                                                                                                                                      QQ
                                                                                                                                                               a
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ò
```

```
SEQUENCE FROM N.A.
SEQUENCE FROM N.A.
MEDLINE=21311952; PubMed=11418146;
MEDLINE=21311952; PubMed=11418146;
Kuroda M., Ohta T., Uchiyama I., Baba T., Yuzawa H., Kobayashi I.,
Cui L., Oguchi A., Aoki K.-I., Nagai Y., Lian J.-O., Ito T.,
Kanamori M., Matsumaru H., Maruyama A., Murakami H., Hosoyama A.,
Mizutani-Ui Y., Takahashi N.K., Sawano T., Inoue R.-I., Kaito C.,
Sekimizu K., Hirakawa H., Kuhara S., Goto S., Yabuzaki J.,
Kanehisa M., Yamashita A., Oshima K., Furuya K., Yoshino C., Shiba T.,
Hattori M., Ogasawara N., Hayashi H., Hiramatsu K.;
"Whole genome sequencing of meticillin-resistant Staphylococcus
aureus.";
Redenbach M., Kieser H.M., Denapaite D., Eichner A., Cullum J., Kinashi H., Hopwood D.A.; March of ordered cosmids and a detailed genetic and physical map for the 8 Mb Streptomyces coelicalor A3(2) chromosome."; Mol. Microbiol. 21:77-96(1996).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Taylor K.
                                                                                                                                                                                                      STRAIN=A3(2) / M145;

STRAIN=A3(2) / M145;

Bentley S.D., Chater K.F., Cerdeno-Tarraga A.-M., Challis G.L.,
Thomson N.R., James K.D., Harris D.E., Quail M.A., Kieser H.,
Harper D., Bateman A., Brown S., Chandra G., Chen C.W., Collins M.,
Cronin A., Fraser A., Goble A., Hidalgo J., Hornsby T., Howarth S.,
Huang C.-H., Kieser T., Larke L., Murphy L., Oliver K., O'Neil S.,
Rabbinowitsch E., Rajandream M.A., Rutherford K., Rutter S.,
Seeger K., Saunders D., Sharp S., Squares R., Squares S., Taylor K.,
Warren T., Wietzorrek A., Woodward J., Barrell B.G., Parkhill J.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       "Complete genome sequence of the model actinomycete Streptomyces
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ;;
0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Staphylococcus aureus (strain N315).
Bacteria; Firmicutes; Bacillus/Clostridium group; Bacillales;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Length 519;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                01-JUN-2001 (TrEMBLrel. 17, Created)
01-JUN-2001 (TrEMBLrel. 17, Last sequence update)
01-JUN-2002 (TrEMBLrel. 21, Last annotation update)
Hypothetical protein SAV1728.
SAV1728 OR SA1549.
Staphylococcus aureus (strain Mu50 / ATCC 700699), and Staphylococcus aureus (strain N315).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Hydrolase; Protease; Serine protease.
SEQUENCE 519 Aa; 50327 MW; 5CB8D5F0CC19E428 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      -1- SIMILARITY: TO SERINE PROTEASES, TRYPSIN FAMILY EMBL; AP003363; BAB57890.1; -. EMBL; AP003134; BAB42817.1; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       3.4%; Score 13; DB 16; I
100.0%; Pred. No. 6.1e-05;
tive 0; Mismatches 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              424 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 coelicolor A3(2).";
Nature 417:41-147(202).
EMBL, AL596251; CAC44701.1; -.
InterPro; IPR00147; PDZ.
InterPro; IPR00145; Ser_Protease_Try.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Lancet 357:1225-1240(2001).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Pfam; PF00595; PDZ; 1.
Pfam; PF00089; trypsin; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Staphylococcus.
NCBI_TaxID=158878, 158879;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Query Match 3.4
Best Local Similarity 100.
Matches 13; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              PRELIMINARY;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        352 QTDASINPGNSGG 364
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   123 QTDASINPGNSGG 135
```

•		
`		4
3		
	•	
)		

SO W SO S

RESULT 13

ò q

```
ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Gaps
                                                                                                                                                                         MEDLINE-95165990; PubMed-7861951;
Tatum F.M., Cheville N.F., Morfitt D.;
"Cloning, characterization and construction of htrA and htrA-like mutants of Brucella abortus and their survival in BALB/c mice.";
Microb Pathog 17:23-36(1994).
EMBL, (007351) AA70163.1;
MEROPS; SOI.273;
       Bacteria; Proteobacturia; gamma subdivision; Enterobacteriaceae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Brucella abortus. >
Bacterla; Proteobacteria; alpha subdivision; Rhizobiaceae group;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Length 464;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Length 474;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        464 AA; .18209 MW; E5D96BF90CFD6542 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       PROSITE; PS50106; PD%; 2.
PROSITE; PS50240; TRYPSIN.DOM; 1.
Hydrolase; Serine Protesses.
SEQUENCE 474 AA; 50159 MW; F74AC9960C4EF9FB CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          01-NOV-1996 (TrEMBLrel. 01, Created)
01-NOV-1996 (TrEMBLrel. 01, Last sequence update)
01-MAR-2002 (TrEMBLrel. 20, Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      3.1%; Score 12; DB 2; Le
100.0%; Pred. No. 0.00068;
ive 0; Mismatches 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     DB 2;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    474 AA
                                                                                                                                                                                                                                                                                                                                          InterPro; IPR001478; PDZ.
InterPro; IPR001940; Protease2C.
InterPro; IPR001254; Ser_protease_Try.
InterPro; IPR00126; Ser_proteas_V8.
Pfam; PF00595; PDZ; 2.
Pfam; PF00089; trypsin; 1.
PRINTS; PR00839; V8PRTEASE.
SMART; SM00228; PDZ; 2.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  3.1%; Score 12;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         InterPro; IPR001478; PDZ.
InterPro; IPR001940; Protease2C.
InterPro; IPR001254; Ser_protease_Try.
Pfam; PF00595; PDZ; 3.
Pfam; PF00089; trypsIn; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    PRT;
                                                                                                                                                    MEDLINE-96239021; PubMed-8675311;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  PROSITE; PS50106; PD2; 2.
PROSITE; PS50240; TRYPSIN_DOM; 1.
Hydrolase; Serine protease.
NON_TER
SEQUENCE 464 AA; 18209 MW; E5
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       PRINTS; PR00834; PROTEASES2C
SMART; SM00228; PDZ; 2.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Local Similarity 100. ses 12; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               PRELIMINARY;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Brucellaceae; Brucella.
NCBI_TaxID=235;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    160 GIGFAIPSNMVK 171
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       SEQUENCE FROM N.A.
                                                                                                      SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            HtrA-like protein.
                                                                                                                                                                                                                                                                                                                        MEROPS; S01.274
                                                     NCBI_TaxID=630;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Best Loca
Matches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   RESULT 15
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        SY WE BREAK 
       ò
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   g
                                                                                                                                                                                                                                                 .;
0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Gaps
                                                                                                                                                                                                                                                      Gaps
                                                                       SMART: SM00228; PDZ; 1.
PROSTIE; PSS0240: TRYPSIN_DOM; 1.
HYDROLASE: Serine protease; Hypothetical protein; Complete proteome.
SEQUENCE 424 AA; 45803 MW; 888ADBA9A6E97948 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              "The Haemophilus influenzae HtrA protein is a protective antigen."; infect. Immun. 66:899-906(1998).
EMBL, AFO18151, AAC38202.1; -.
MEROPS, S01.274, -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       MEDLINE-98147697; PubMed-9488373;
Loosmore S.M., Yang Y.P., Oomen R., Shortreed J.M., Coleman D.C.,
                                                                                                                                                                                                                                                 ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ò
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Haemophilus influenzae.
Bacteria: Proteobacteria: gamma subdivision; Pasteurellaceae;
Haemophilus.
                                                                                                                                                                                                  Length 424;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       3.1%; Score 12; DB 2; Length 437; 100.0%; Pred. No. 0.00064; Live 0; Mismatches 0; Indels
                                                                                                                                                                                             Query Match 3.1%; Score 12; DB 16; Length 42 Best Local Similarity 100.0%; Pred. No. 0.00062; Matches 12; Conservative 0; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      437 AA; 46376 MW; 27AE2E9F27BE5F6C CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 01-AUG-1998 (TrEMBLrel. 07, Created)
01-AUG-1998 (TrEMBLrel. 07, Last sequence update)
01-MAR-2002 (TrEMBLrel. 20, Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Last sequence update)
Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                     437 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       464 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Interpro: IPR001314; Chymotrypsin.
Interpro: IPR001478; Pb2.
Interpro: IPR00140; Protease2C.
Interpro: IPR001244; Ser_protease_Try.
Pfam; PF00585; pb2; 2.
Pfam; PF00899; trypsin; 1.
PRINTS: PR00891; CHYMOTRYPSIN.
PRINTS: PR00834; PROTEASES2C.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Created)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                     PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     PROSITE; PS50106; PD2; 2.
PROSITE; PS50240; TRYPSIN_DOM; 1.
Hydrolase; Serine protease.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             5845

, Q56885

T .01-NOV-1996 (TrEMBLrel. 01, Cr.

) T .01-NOV-1996 (TrEMBLrel. 01, Le

) T .01-NOV-1996 (TrEMBLrel. 21, L.
Pfam; PF00595; PD2; 1.
Pfam; PF00089; trypsin; 1.
PRINTS; PR00834; PROTEASES2C.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                     PRELIMINARY;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Best Local Similarity 100.
Matches 12; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Yersinia enterocolitica.
                                                                                                                                                                                                                                                                                                                           138 YIVTNNHVIDGA 149
                                                                                                                                                                                                                                                                                               22 YIVTNNHVIDGA 33
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   SMART; SM00228; PDZ;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        25 TNNHVIDGADKI 36
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    88 TNNHVIDGADKI 99
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     NCBI_TaxID=727;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              HtrA (Fragment)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Klein M.H.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         SEQUENCE
                                                                                                                                                                                                Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          068197;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                   068197
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        RESULT 14
10 05687
AC 0568
DT 01:
DT 0
DE GN
                                                                                                                                                                                                                                              Matches
```

ě			
•			
· .			*,

Gaps

ö

Length 476;

DB 16; I

Query Match
Best Local Similarity 100.
Matches 96; Conservative

SMART; SM00228; PD2; 2.
PROSITE; PS50106; PDZ; 2.
PROSITE; PS50400 'FRYPSIL DOM; 1.
HYDROLASE, Serine protesse; Complete proteome.
SEQUENCE 476 AA; 51713 MW; 4E338AED839BFE18 CRC64;

DR DR WW SQ

174 VTQLIKTGKIERGYLGVGLQDLSGDLQNSYDNKEGAVVISVEKDSPAKKAGILVWDLITE 233

g

```
ö
                                                                                                                                                                                                                                                                                                                                                                                                    61 AVIRITKDNLPTIKFSDSNDISVGDLVFALGNPFGVGESVTQGIVSALNKSGIGINSYEN 120
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               GKIERGYLGVGLQDLSGDLQNSYDNKEGAVVISVEKDSPAKKAGILVWDLITEVNGKKVK 240
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                FIQTDASINPGNSGGALIDSRGGLVGINTAIISKTGGNHGIGFAIPSNMVKDTVTQLIKT 180
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      NTNELRNLIGSMLPNQRVTLKVIRDKKERAFTLTLAERKNPNKKETISAQNGAQGQLNGL 300
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     QVEDLTQETKRSMRLSDDVQGVLVSQVNENSPAEQAGFRQGNIITKIEEVEVKSVADFNH 360
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            1 MIPKERMERALGSGVIISKDGYIVTNNHVIDGADKIKVTIPGSNKEYSATLVGTDSESDL 60
                                                                                                                                                                                                                                                                                                                              0; Gaps
Tomb- etakgt
                                                                                                                                                                                                                                                                      DB 16; Length 443;
                                                                                               PROSITE; PS50106; PD2, 2.
PROSITE; PS50240; TRYPSIN_DOM; 1.
Hydrolase; Hypothetical protein; Protease; Serine protease;
                                                                                                                                                                                                                                                                                                                            Indels
                                                                                                                                                                                                              443 AA; 47983 MW; 03FDDBD72CF31EE2 CRC64;
                                                                                                                                                                                                                                                                                                                         ó
                                                                                                                                                                                                                                                                    ; Score 387; DB; Pred. No. 0; O; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                01-WAY-1999 (TrEMBLrel. 10, Created)
01-WAY-1999 (TrEMBLrel. 10, Last seq
01-JUN-2002 (TrEMBLrel. 21, Last anno
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        361 ALEKYKGKPKRFLVLDLNQGYRIILVK 387
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       417 ALEKYKGKPKRFLVLDLNQCYRIILVK 443
                                                                                                                                                                                                                                                                    100.0%;
                                                                                                                                                                                                                                                                                          Best Local Similarity 100.0
Matches 387; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   PRELIMINARY;
                                                                           $M00228; PDZ; 2.
                                                                                                                                                                                     Complete proteome.
SEQUENCE 443 AA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Q92M18
Q92M18;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           297
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   357
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          121
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  181
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                301
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         241
     立
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 RESULT 2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          092M18
                                                                                                                                                                                                                                                                                                                                                                                                                        QQ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ò
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               g
                                                                                                                                                                                                                                                                                                                                                                           ò
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ò
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       8
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ŏ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 a
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ò
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      q
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ò
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   g
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Q
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      HDD REAR AND DESTRUCTION OF THE PROPERTY OF TH
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ò
```

```
;
0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Gaps
                                                                                                                                                                                                                                                                                                                                   Bacteria; Proteobacteria; epsilon subdivision; Campylobacter group;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Taylor D.E., Hiratsuka K.; "Use of non-radioactive DNP probes for detection of Campylobacter jejuni and Campylobacter coli in stool specimens."; Mol. Cell. Probes 4:261-271(1990).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Length 368;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Submitted (MAY-1995) to the EMBL/GenBank/DDBJ databases.
EMBL; U27271], AAA68943.1; -.
MEROPS; S01.273; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             368 AA; 39491 MW; CFA14B08EE49EF70 CRC64;
                                                                                                                             01-NOV-1996 (TrEMBLrel. 01, Created)
01-NOV-1996 (TrEMBLrel. 01, Last sequence update)
01-MAR-2002 (TrEMBLrel. 20, Last annotation update)
Heat shock protein/serine protease (Fragment).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       5.2%; Score 20; DB 2; Lk
100.0%; Pred. No. 9.5e-13;
Live 0; Mismatches 0;
                                                                          368 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               472 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             InterPro; IPR001478; PDZ.
InterPro; IPR001478; PDZ.
InterPro; IPR001344; PDZ.
InterPro; IPR001344; Ser_Protease_Try.
Pfam; PF00595; PDZ; Z.
Pfam; PF00089; trypsin; 1.
PRINTS; PR00834; FROTEASES.Z.
SMART; SM00228; PEZ; Z.
PROSITE; PS50106; PDZ; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Hydrolase; Protease; Serine protease.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 MEDLINE=90384493; PubMed=2402249;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 106 YENFIQTDASINFGNSGGAL 125
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           118 YENFIQTDASINFGNSGGAL 137
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Conservative
                                                                       PRELIMINARY;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               PRELININARY;
                                                                                                                                                                                                                                                                                                 Campylobacter jejuni
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                 SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                SEQUENCE FROM N.A. STRAIN-UA580;
                                                                                                                                                                                                                                                                                                                                                              Campylobacter.
NCBI_TaxID-197;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   STRAIN-UA580
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Hiratsuka K.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Q46120
Q46120;
                                                                                                         046094;
                                                                       046094
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Matches
RESULT 3
Q46094
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           RESULT 4
Q46120
                                                                       DDT THE SECTION OF SEC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               δλ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         g
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            AC AC
```

SEQUENCE FROM N.A.
MEDLINE-99120557; AALD M.A.
MEDLINE-99120557; Pubmed-9923682;
Moir D.T., King B.L., Brown E.D., Doig P.C.,
Smith D.R., Noonan B., Guild B.C., deJonge B.L., Carmel G.,
Tummino P.J., Caruso A., Uria Nickelsen M., Mills D.M., Ives C.,
Gibson R., Merberg D., Mills S.D., Jiang Q., Taylor D.E., Vovis G.F.,

Helicobacter pylori J99 (Campylobacter pylori J99). Bacteria; Proteobacteria; epsilon subdivision; Helicobacter group; Helicobacter.

NCBI_TaxID=85963;

Protease DO. HTRA OR JHP0405.

Last sequence update) Last annotation update)

Genomic sequence comparison of two unrelated isolates of the human

InterPro; IPR001478; PDZ.
InterPro; IPR001940; Protease2C.
InterPro; IPR001254; Ser_Protease_Try.
Pfam; PF000595; PDZ; 1.
Pfam; PF00089; trypsin; 1.
PRINTS; PR00834; PROTEASES2C.

			•	**************************************
	•			
			24 . ·	
\$.			· * *	
	*	•		¥
2.5				
			a di	* •.* · · ·
			1	,
		i No bi		
	**			y.
A P				
		7 7 1	. 3	(*)
				· · · · · · · · · · · · · · · · · · ·
a constant				
	*			
				t = t
				· ·
Y				*
*	*			
L	and the same stead of	The second second		•

us-09-895-913a-120 2.ran

```
GenCore version 5.1.3
Copyright (c) 1993 - 2002 Compugen Ltd.
```

OM protein - protein search, using sw model

November 18, 2002, 11:29:46; Search time 11 Seconds Run on:

(without alignments) 529.869 Million cell updates/sec

US-09-895-913A-120 Perfect score:

1 MIPKERMERALGSGVIISKD............KPKRFLVLDLNQGYRIILVK 387 BLOSUM62 Gapop 10.0 , Gapext 0.5 Scoring table: Sequence:

97044 seqs, 15060890 residues Searched:

97044 Total number of hits satisfying chosen parameters:

Minimum DB seq length: 0 Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0% Maximum Match 100% Listing first 45 summaries

Published_Applications_AA:*

/cgn2_6/ptodata/1/pubpaa/US08_NEW_PUB.pep:* /cgn2_6/ptodata/1/pubpaa/PCT_NEW_PUB.pep:* /cgn2_6/ptodata/1/pubpaa/US06_NEW_PUB.pep:* Database :

'cgn2_6/ptodata/1/pubpaa/USO6_PUBGCOMB.pep:*
'cgn2_6/ptodata/1/pubpaa/USO6_PUBGCOMB.pep:*
'cgn2_6/ptodata/1/pubpaa/USO7_PUBGCOMB.pep:*
'cgn2_6/ptodata/1/pubpaa/USO9_PUBCOMB.pep:*
'cgn2_6/ptodata/1/pubpaa/USO9_NEW_PUB.pep:*
'cgn2_6/ptodata/1/pubpaa/USO9_NEW_PUB.pep:*
'cgn2_6/ptodata/1/pubpaa/USO9_NEW_PUB.pep:*
'cgn2_6/ptodata/1/pubpaa/USO9_NEW_PUB.pep:*
'cgn2_6/ptodata/1/pubpaa/USO9_UBGCOMB.pep:*
'cgn2_6/ptodata/1/pubpaa/USO9_UBGCOMB.pep:*
'cgn2_6/ptodata/1/pubpaa/USO9_UBGCOMB.pep:*
'cgn2_6/ptodata/1/pubpaa/USO0_PUBCOMB.pep:*
'cgn2_6/ptodata/1/pubpaa/USO0_PUBCOMB.pep:* 117::... 112::... 14::::...

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result		Query		;	
Score	- :	Length	98	QI.	Description
1938	8 100.0	387	σ	US-09-895-913A-120	Sequence 120, App
16.		503	10	US-09-752-385-8	Sequence 8, Appli
84.		447	10	US-09-388-089B-2	Sequence 2, Appli
84.		475	10	US-09-388-089B-12	Sequence 12, Appl
84.		498	10	US-09-388-089B-11	Sequence 11, Appl
45		549	σ	US-09-712-363-190	Sequence 190, App
38		464	σ	US-09-712-363-182	Sequence 182, App
55.		286	10	US-09-764-898-256	Sequence 256, App
340.5		476	10	US-09-935-390A-37	Sequence 37, Appl
28		330	10	US-09-764-898-184	Sequence 184, App
281.		355	6	US-09-712-363-161	Sequence 161, App
21		296	10	US-09-287-849-26	Sequence 26, Appl
21		729	10	US-09-287-849-2	Sequence 2, Appli
147.		397	σ	US-09-712-363-280	Sequence 280, App
13		3241	10	US-09-841-786-1	Sequence 1, Appli
12		204	10	US-09-925-300-1397	Sequence 1397, Ap
26.		369	10	US-09-841-786-2	Sequence 2, Appli
12		2037	10	US-09-951-401-3	Sequence 3, Appli
12		2037	10	US-09-922-101-3	Sequence 3. Appli

	Sequence 6, Appli	Sequence 6, Appli	Sequence 4, Appli	Sequence 179, App	Sequence 6, Appli	Sequence 4, Appli	Seguence 9, Appli	Sequence 10, Appl	Sequence 304, App	Sequence 2, Appli	Sequence 4, Appli	Sequence 34281, A	Sequence 33, Appl	Sequence 302, App	Sequence 5352, Ap	Sequence 12278, A	Sequence 11037, A	Sequence 32, Appl	Sequence 2, Appli	Sequence 59, Appl	Sequence 3, Appli	Sequence 5824, Ap	Sequence 12997, A	Sequence 10779, A	Sequence 11558,	Sequence 63, Apply	
	10 US-09-841-786-6	10 US-09-823-356-6	10 US-09-740-027-4	12 US-10-001-843-179	10 US-09-813-820-6	10 US-09-841-786-4	9 US-10-092-880-9	9 US-10-092-880-10	10 US-09-741-669-304	9 US-10-092-880-2	9 US-10-092-880-4	10 US-09-864-761-34281	10 US-09-797-862-33	10 US-09-912-020-302	10 US-09-815-242-5352	10 US-09-815-242-12278	10 US-09-815-242-11037	10 US-09-797-862-32	10 US-09-800-065-2	10 US-09-919-497-59	10 US-09-841-786-3	10 US-09-815-242-5824	10 US-09-815-242-12997	10 US-09-815-242-10779	10 US-09-815-242-11568	9 US-10-121-032-63	
	773	358	358	434	512	714	1599	1600	1325	1536	1477	68	2353	2383	239	253	1343	1098	619	767	927	887	887	930	692	926	
	6.4	6.3	6.3	6.3	6.3	0.9	0.9	0.9	5.9	5.9	5.9	5.9	5.8	5.8	5.8	5.8	5.8	5.7	5.6	2.6	5.5	5.5	5.5	5.5	5.4	5.4	
	123.5	122	122	122	122	117	115.5	115.5	115	115	114.5	113.5	113	112	111.5	111.5	111.5	110.5	109	108	107.5	106	106	106	105.5	105.5	
100	120	21	22	23	24	25	26	27	28	29	30	31	32	33	34	35	36	37	38	39	40	41	42	43	44	45	

ALIGNMENTS

```
APPLICANT: Al-Garawi, Amal APPLICANT: Miler, Charles APPLICANT: Miler, Charles APPLICANT: Tomb, Jean Francois APPLICANT: Tomb, Jean Francois APPLICANT: Tomb, Jean Francois TITLE OF INVENTION: Identification of Polynucleotides TITLE OF INVENTION: Encoding No. US20020160456Alel Helicobacter Polypeptides in TITLE OF INVENTION: Genome FILE REFERENCE: 06132/043002 CURRENT APPLICATION NUMBER: US/09/895,913A CURRENT APPLICATION NUMBER: US/09/895,913A CURRENT FILING DATE: 1997-06-29 PRIOR FILING DATE: 1997-06-24 NUMBER OF SEQ ID NOS: 368 SEC ID NOS: 368 SEC ID NO 120 LENGTH: 387
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ő
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            61 AVIRITKDNLPT: (KFSDSNDISVGDLVFAIGNPFGVGESVTQGIVSALNKSGIGINSYEN 120
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       1 MIPKERMERALGSGVIISKDGYIVTNNHVIDGADKIKVTIPGSNKEYSATLVGTDSESDL 60
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             1 MIPKERMERALGSGVIISKDGYIVTNNHVIDGADKIKVTIPGSNKEYSATLVGTDSESDL 60
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ;
0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               100.0%; Score 1938; DB 9; Length 387; 100.0%; Pred. No. 2.1e-140; ive 0; Mismatches 0; Indels 0
                     Sequence 120, Application US/09895913A Patent No. US20020160456A1 PATENT INFORMATION: APPLICANT: Kleanthous, Harold
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ORGANISM: Helicobacter pylori
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Best Local Similarity 100.
Matches 387; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    US-09-895-913A-120
US-09-895-913A-120
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 g
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               οy
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          g
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Óγ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ò
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         g
```

~

à 쉽 ò g ŏ qq

g

ŏ

```
245
                                                                                                                                                                                  246 RNLIGSMLPNORVTLKVIRDKKERAFTLTLAERKNPNKKETISAONGAOGOLNGLOVEDL 305
                                                                                                                                                                                                                  411
                                                                                                                                                                                                                                                                    62 IPQEEADDGGLNFGSGFIISKDGXILTNTHVVTGMGSIKVLL-NDKREYTAKLIGSDVQS 120
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   292
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    INPGNSGGALIDSRGGLVGINTAIISKTGGNHGIGFAIPSNMVKDTVTQLIKTGKIERGY 187
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  DLAVIRI-TKDNLPTIKFSDSNDISVGDLVFAIGNPFGVGESVTQGIVSALNKSGIGINS 117
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   118 YENFIQTDASINPGNSGGALIDSRGGLVGINTAIISKTGGNHGIGFAIPSNMVKDTVTQL 177
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                178 IKTGKIERGYLGVGLQDLSGDLQNSY - DNKEGAVVISVEKDSPAKKAGILVWDLITEVN 235
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Pacente No. US20020018782A1
GENERAL INFORMATION:
APPLICAMT: Jackson, W.
APPLICAMT: Jackson, W.
TITLE OF INVENTION: SEQUENCE AND USES THEREOF
FILE REPERENCE: 7969-083
CURRENT APPLICAND NUMBER: US/09/388,089B
CURRENT APPLICAND NOW.
 188 LGVGLQDLSGDLQNSYDNKE--GAVVISVEKDSPAKKAGILVWDLITEVNGKKVKNTNEL
                                                                                                                                                                                                                                                 306 TQETKRSMRL----SDDVQGVLVSQVNENSPAEQAGFRQGNIITKIEEVEVKSVADFNHA
                                                                                                                                     | : | | : | | : | | 361 AKRIANMSPGETVTLGVWKSGKEENIKVKLDSMPEDENMKDGSKYSNEHGN-----
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  2 IPKERMERA---LGSGVIISKDGYIVTNNHVIDGADKIKVTIPGSNKEYSATLVGTDSES
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   GKKVKNTNELRNLIGSMLPNQRVTLKVIRDKKERAFTLTL----AERKNPNKKETISAQNG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    AQGQLNGLQVEDLTQETKRSMRLSDDVQGVLVSQVNENSPAEQAGFRQGNITTKIEEVEV
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   19;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Length 447;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   DB 10;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   30.2%; Score 584.5; DB 10;
ilarity 37.3%; Pred. No. 2.8e-37;
Conservative 78; Mismatches 143;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                KSVADFNHALEKYKGKPKRFLVL 375
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Patentin Ver. 2.0
                                                                                                                                                                                                                                                                                                                LEKYKGKPKRFLVLDL 377
                                                                                                                                                                                                                                                                                                                                        472 IKNAQKLGRKAILLQV 487
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ORGANISM: Neisseria spp
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Query Match
Best Local Similarity
Matches 143; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                    US-09-388-089B-2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    447
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    US-09-388-089B-2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    SOFTWARE:
SEQ ID NO 2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    LENGTH:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   29
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  121
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  179
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   239
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   236
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  299
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   293
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                359
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  353
                                                                                                                                                 셤
                                                                                                                                                                                                                g
                                                                                                                                                                                                                                                                                   g
                                                                                g
                                                                                                                 ò
                                                                                                                                                                                   ò
                                                                                                                                                                                                                                                   ò
                                                                                                                                                                                                                                                                                                                    ò
                                                                                                                                                                                                                                                                                                                                               셤
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 g
                                                   á
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ò
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  g
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ò
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                g
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ŏ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 g
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ò
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                g
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              g
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ò
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    .;
8
300
                                                                                                                                Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               10 ALGSGVIISKDGYIVTNNHVI-DGADKIKVTIPGSNKEYSATLVGTDSESDLAVIRIT-K 67
                                                                                                                                                                                                                                                                                                                                                                     APPLICANT: AUGUSTON, 2007. RESPICT, RUSSELL L
TITLE OF INVENTION: Nucleic Acids of Rochalimaea Henselae
                                                                                                                                                                                                                                                                                                                                                                                                                                                 Henselae and Rochalimaea Quintana Infection
                                                                 NTNELRNLIGSMLPNORVTLKVIRDKKERAFTLTLAERKNPNKKETISAQNGAQGQLNGL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              68 DNLPTIKFSDSNDISVGDLVFAIGNPFGVGESVTQGIVSALNKSGIGINSYENFIQTDAS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                21;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Length 503;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ADDRESSEE: NEEDLE & ROSENBERG, P.C.
STREET: 127 Peachtree Street, N.E., Suite 1200
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   25
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            COMPUTER READBLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: 1BM PC compatible
COMPUTER: SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 DB 10;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                145;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Score 616.5; DB 1
Pred. No. 1.2e-39;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              NAME: Spratt, Gwendolyn D.
REGISTRATION NUMBER: 36,016
REFERENCE/DOCKET NUMBER: 1141.624
TELECOMMUNICATION INFORMATION:
TELEPRONE: (404) 688-0770
INFORMATION FOR SEQ ID NO: 8:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                63; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/752,385
FILING DATE: 29-Dec-2000
CLASSIFICATION: <a href="https://doi.org/10.1007/com/">doi.org/10.1007/com/</a>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 PRIOR APPLICATION DATA:
APPLICATION NUMBER: 09/525,310
FILING DATE: <UNKnown>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   œ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               TOPOLOGY: linear
MOLECULE TYPE: protein
SEQUENCE DESCRIPTION: SEQ ID NO:
                                                                                                                                                                                                 361 ALEKYKGKPKRFLVLDLNQGYRIILVK 387
                                                                                                                                                                                                                  Rochalimaea
                                                                                                                                                                                                                                                                                                               Sequence 8, Application US/09752385
Patent No. US20020012919A1
GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                LENGTH: 503 amino acids TYPE: amino acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 31.8%;
39.1%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                  SEQUENCES: 14
                                                                                                                                                                                                                                                                                                                                                                                                                                                                NUMBER OF SEQUENCES: 14
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Query Match 31.89
Best Local Similarity 39.19
Matches 147; Conservative
                                                                                                                                                                                                                                                                                                                                                                  APPLICANT: Anderson,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 STATE: Georgia
COUNTRY: USA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   CITY: Atlanta
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ZIP: 30303
                                                                                                                                                                                                                                                                                  RESULT 2
US-09-752-385-8
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 US-09-752-385-8
                                  181
                                                                                                                                                                                                                                361
                                                                  241
181
```

g

õ

δ

10;

```
US-09-388-089B-11
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       US-09-712-363-190
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                SOFTWARE: Fas
SEQ ID NO 190
LENGTH: 549
TYPE: PRT
                  ORGANISM:
                                                                                                                                                                                              29
                                                                                                                                                                                                                                                                                                                                                                                           236
                                                                                                                                                              g
                                                                                                                                                                                              δy
                                                                                                                                                                                                                           q
                                                                                                                                                                                                                                                           δy
                                                                                                                                                                                                                                                                                        g
                                                                                                                                                                                                                                                                                                                           δ
                                                                                                                                                                                                                                                                                                                                                        g
                                                                                                                                                                                                                                                                                                                                                                                           ò
                                                                                                                                                                                                                                                                                                                                                                                                                        d
                                                                                                                                                                                                                                                                                                                                                                                                                                                          ŏ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      q
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ŏ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     g
                                                                                                                                                                                                                                                                                                                                                                                                                          10;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           118 YENFIQTDASINPGNSGGALIDSRGGLVGINTAIISKTGGNHGIGFAIPSNMVKDTVTQL 177
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       178 IKTGKIERGYLGVGLQDLSGDLQNSY--DNKEGAVVISVEKDSPAKKAGILVWDLITEVN 235
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        59 DLAVIRI-TKDNLPTIKFSDSNDISVGDLVFAIGNPFGVGESVTQGIVSALNKSGIGINS 117
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     GKKVKNTNELRNLIGSMLPNQRVTLKVIRDKKERAFTLTL---AERKNPNKKETISAQNG 292
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  AQGQLNGLQVEDLTQETKRSMRLSDDVQGVLVSQVNENSPAEQAGFRQGNIITKIEEVEV 352
                                                                                                                                                                                                                                                                                                                                                                                                                           Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                      2 IPKERMERA---LGSGVIISKDGYIVTNNHVIDGADKIKVTIPGSNKEYSATLVGTDSES 58
                                                                                    Sequence 12, Application US/09388089B
Patent No. US20020018782A1
GENERAL INFORMATION:
APPLICANT: Jackson, W.
APPLICANT: Harris, A.
TITLE OF INVENTION: SEQUENCE AND USES THEREOF
FILE REFERENCE: 7969-083
CURRENT APPLICATION NUMBER: US/09/388,089B
CURRENT FILING DATE: 1999-08-31
NUMBER OF SEQ ID NOS: 20
SOFTWARE: Patentin Ver. 2.0
SEQ ID NO 12
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Sequence 11, Application US/09388089B
Patent No. US20020018782A1
GENERAL INFORMATION:
APPLICANT: Jackson, W.
APPLICANT: Harris, A.
TITLE OF INVENTION: NEISSERIA MENINGITIDIS POLYPEPTIDE, NUCLEIC ACID
TITLE OF INVENTION: SEQUENCE AND USES THEREOF
FILE REPERENCE: 7969-083
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  GGEIRSSGDLPVMVGAITPGKEVSLGVWRKGEEITIKVKLGNAAEHIGASSKTDEAPYTE
                                                                                                                                                                                                                                                                                                                                                                                                                          19;
                                                                                                                                                                                                                                                                                                                                                                                                                        Indels
                                                                                                                                                                                                                                                                                                                                                                                      30.2%; Score 584.5; DB 10; 37.3%; Pred. No. 3e-37; tive 78; Mismatches 143;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             FILE REFERENCE: 7969-083
CURRENT APPLICATION NUMBER: US/09/388,0898
CURRENT FILING DATE: 1999-08-31
NUMBER OF SEQ ID NOS: 20
SOFTWARE: Patentin Ver. 2.0
SEQ ID NO 11
LENGTH: 498
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               441 NDEAGFRKAMDK-AGKNVPLLIM 462
| | | |::| || |::
NDEAGFRKAMDK-AGKNVPLLIM 434
                                                                                                                                                                                                                                                                                                                                         ORGANISM: Neisseria meningitidis
                                                                                                                                                                                                                                                                                                                                                                                                       Best_Local Similarity 37.3
Matches 143; Conservative
                                                                           US-09-388-089B-12
                                                                                                                                                                                                                                                                                                                                                        US-09-388-089B-12
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               US-09-388-089B-11
                                                                                                                                                                                                                                                                                                                         TYPE: PRT
               413
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     149
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   207
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   267
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     236
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  293
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    327
               g
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      셤
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   g
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     δ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  g
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   δ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  g
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               q
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ä
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   셤
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ò
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  à
```

```
10;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              350 GGEIRSSGDLPVMVGAITPGKEVSLGVWRKGEEITIKVKLGNAAEHIGASSKTDEAPYTE 409
                                                                                                                                                                                                                                                  DLAVIRI-TKDN: PTIKFSDSNDISVGDLVFAIGNPFGVGESVTQGIVSALNKSGIGINS 117
                                                                                                                                                                                                                                                                                                                                                                                                                                                              118 YENFIQTDASINPGNSGGALIDSRGGLVGINTALISKTGGNHGIGFAIPSNMVKDTVTQL 177
                                                                                                                                                    Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         DETERMINING THE FUNCTIONS AND INTERACTIONS OF PROTEINS BY COMPARATIVE ANALYSIS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 290 KNTGKVQRGQLGVIIQEVSYGLAQSFGLDKAGGALIAKILPGSFAERAGLRAGDIVLSLD
                                                                                                                                                                                                                                                                                                                                                                             178 IKTGKIERGYLGYGLQDLSGDLQNSY--DNKEGAVVISVEKDSPAKKAGILVWDLITEVN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   GKKVKNTNELRN; IGSMLPNQRVTLKVIRDKKERAFTLTL---AERKNPNKKETISAQNG
                                                                                                                                                                                                              2 IPKERMERA---JGSGVIISKDGYIVTNHVIDGADKIKVTIPGSNKEYSATLVGTDSES
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           293 AQGQLNGLQVEDLTQETKRSMRLSDDVQGVLVSQVNENSPAEQAGFRQGNIITKIEEVEV
                                                                                                                                                 19;
                                                                                       Length 498;
                                                                                    Query Match 30.2%; Score 584.5; DB 10; Length Best Local Similarity 37.3%; Pred. No. 3.2e-37; Matches 143; Conservative 78; Mismatches 143; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         APPLICANI: MAIOCOLE, EGWARD M.
TITLE OF INVERTION: DETERMINING THE FUNCTIONS
TITLE OF INVERTION: INTERACTIONS OF PROTEIN
FILE REFERENCE: 07419-03201
GURRENT APPLICATION NUMBER: 02/0712,363
CURRENT FILING DATE: 2000-11-13
PRIOR APPLICATION NUMBER: 60/179,531
PRIOR APPLICATION NUMBER: 60/179,531
PRIOR APPLICATION NUMBER: 60/179,531
PRIOR APPLICATION NUMBER: 60/118,206,
PRIOR FILING DATE: 1999-01-29
PRIOR FILING DATE: 1999-01-29
PRIOR FILING DATE: 1999-01-29
PRIOR FILING DATE: 1999-02-01
PRIOR FILING DATE: 1999-02-01
PRIOR FILING DATE: 1999-03-26
PRIOR APPLICATION NUMBER: 60/134,093
PRIOR APPLICATION NUMBER: 60/134,093
PRIOR APPLICATION NUMBER: 60/134,093
PRIOR APPLICATION NUMBER: 60/144,092
PRIOR APPLICATION NUMBER: 60/15,124
PRIOR APPLICATION NUMBER: 60/165,124
PRIOR FILING DATE: 1999-11-12
PRIOR FILING DATE: 1999-11-12
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                NUMBER OF SEQ ID NOS: 292
SOFTWARE: FastSEQ for Windows Version 4.0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Sequence 190, Application US/09712363
Patent No. US20020164588A1
GENERAL INFORMATION:
APPLICANT: Eisenbery, David
APPLICANT: Rotstein, Sergio H.
APPLICANT: Marcottè, Edward M.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  353 KSVADFNHALEKYKGKPKRFLVL 375
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         464 NDEAGFRKAMDK-AGKNVPLLIM 485
Neisseria meningitidis
```

```
181 GSGIILSAEGLILTNNHVIAAAAKPPLGSPPPKTTVTFSDGRTAPFTVVGADPTSDIAVV 240
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Ouery Match
Best Local Similarity 33.19
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 . . . . . . . . . . . . .
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ORGANISM: Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           NAME/KEY: SITE
LOCATION: (35)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      NAME/KEY: SITE
                                                                                                                                                                                                                                                                                                                                                                               RESULT 8
US-09-764-898-256
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      SEQ ID NO 256
LENGTH: 286
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      LOCATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         LOCATION:
                                                                                                                    117
                                                                                                                                                                                                                                                                               230
                                                                                                                                                                                                                                                                                                                    413
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      99
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    122
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             178
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    182
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           230
                                                                             g
                                                                                                                                                         g
                                                                                                                                                                                                 ò
                                                                                                                                                                                                                                        g
                                        à
                                                                                                                    ò
                                                                                                                                                                                                                                                                               ŏ
                                                                                                                                                                                                                                                                                                                qq
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                g
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        à
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             엄
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ò
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       g
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ŏ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  g
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         õ
                                                                                                    9
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ..
8
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              APPLICANT: Elsenberg, David
APPLICANT: Rotstein, Sergio H.
APPLICANT: Rotstein, Sergio H.
APPLICANT: Marcontte, Edward M.
TITLE OF INVENTION: DETERMINING THE FUNCTIONS BY COMPARATIVE ANALYSIS
TITLE OF INVENTION: INTERACTIONS OF PROTEINS BY COMPARATIVE ANALYSIS
TITLE REFERENCE: 07419-032001
CURRENT APPLICATION NUMBER: 0700-01-28
FRIOR APPLICATION NUMBER: 60/112,831
FRIOR PILLING DATE: 2000-01-28
FRIOR PILLING DATE: 2000-01-28
FRIOR FILLING DATE: 1999-01-29
FRIOR FILLING DATE: 1999-01-29
FRIOR FILLING DATE: 1999-02-01
FRIOR PELICATION NUMBER: 60/118,206,
FRIOR PELICATION NUMBER: 60/114,093
FRIOR APPLICATION NUMBER: 60/134,093
FRIOR APPLICATION NUMBER: 60/134,093
FRIOR APPLICATION NUMBER: 60/134,093
FRIOR PILLING DATE: 1999-05-14
FRIOR FILLING DATE: 1999-05-14
FRIOR FILLING DATE: 1999-05-14
FRIOR FILLING DATE: 1999-05-14
FRIOR FILLING DATE: 1999-01-1-12
FRIOR FILLING DATE: 1999-01-1-12
FRIOR FILLING DATE: 1999-11-1-12
FRIOR APPLICATION NUMBER: 60/165,086
FRIOR FILLING DATE: 1999-11-1-12
FRIOR APPLICATION NUMBER: 60/165,086
FRIOR FILLING DATE: 1999-11-1-12
FRIOR FILLING DATE: 1999-11-1-12
FRIOR FILLING DATE: 1999-11-1-12
                                                                                                                                                             67 K-DNLPTIKFSDSNDISVGDLVFAIGNPFCVGESVTQGIVSALNK-----SGIGINSYE 119
                                                                                                                                                                                                                                            120 NFIQTDASINPGNSGGALIDSRGGLVGINTALISKTGGNHGIGFAIPSNMVKDTVTQLIK 179
                                                                                                 Gaps
                                                                                                                                      12 GSGVIISKDGYIVTNNHVIDGA----DKIKVTIP-GSNKEYSATLVGTDSESDLAVIRIT 66
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           12 GSGVIISKDGYIVTNNHVIDGADK-----IKVTIPGSN-KEYSATLVGTDSESDLAVI 63
                                                                                                                                                                                                                                                                                                                      180 TGKIERGYLGVGLQDLSGDLQNSYDNKEGAVVISVEKDSPAKKAGILVWDLITEVNGKKV
                                                                                                 22;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    30;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Query Match 19.9%; Score 386; DB 9; Length 464; Best Local Similarity 38.0%; Pred. No. 3.8e-22; Matches 103; Conservative 42; Mismatches 96; Indels
                                                           Length 549;
                                                                                                 Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                        240 KNTNELRNLIGSMLPNQRVTLKVIRDKKERAFTLTLAERKNPN 282
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 509 ADSDEFVVAVRQLAIGQDAPIEVVREGRH----VTLTVKPDPD 547
                                                                                                 66
                                                         ; Score 459; DB 9;
; Pred. No. 1.3e-27;
49; Mismatches 99
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    NUMBER OF SEQ ID NOS: 292
SOFTWARE: FastSEQ for Windows Version 4.0
  ; ORGANISM: Mycobacterium tuberculosis US-09-712-363-190
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Mycobacterium tuberculosis
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Sequence 182, Application US/09712363 Patent No. US20020164588A1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               23.7%;
39.9%;
                                                                             Best_Local Similarity 39.9
Matches 113; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      GENERAL INFORMATION
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             US-09-712-363-182
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             SEQ ID NO 182
LENGTH: 464
                                                             Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    TYPE: PRT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ORGANISM:
                                                                                                                                                                           g
                                                                                                                                                                                                                                                         g
                                                                                                                                                                                                                                                                                                 δ
                                                                                                                                                                                                                                                                                                                                      g
                                                                                                                                                                                                                                                                                                                                                                                                              ·
연
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             g
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ŏ
                                                                                                                                        à
                                                                                                                                                                                                                      ö
                                                                                                                                                                                                                                                                                                                                                                             ð
                                                                                                                                                                                                                                                                                                                                                                                                                                                        ò
```

```
10;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ; LOCATION: (104)
; OTHER INFORMATION: Xaa equals any of the naturally occurring L-amino acids
US-09-764-898-256
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          LOCATION: (32)
OTHER INFORMATION: Xaa equals any of the naturally occurring L-amino acids
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              OTHER INFORMATION: Xaa equals any of the naturally occurring L-amino acids NAME/KEY: SITE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 OTHER INFORMATION: Xaa equals any of the naturally occurring L-amino acids
                                                                                                                                         SYENFIQTDASINPGNSGGALIDSRGGLVGINTAIIS-----KTGGNHGIGFAIPSNM 169
                                                                                                                                                                                                                    170 VKDTVTQLIKTGKIERGYLGVGLQDLSGDLQNSYDNKEGAVVISVEKDSPAKKAGILVWD 229
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         RIT-KDNLPTIKFSDSNDISVGDLVFAIGNPFGVGESVTQGIVSALNK--SGIG----IN 116
                                                                                                                                                                                                                                                                          361 AKRIADELISTGKASHASLGV-----QVTNDKDTL-GAKIVEVVAGGAAANAGVPKGV 412
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         -TKDNLPTIKFSDSNDISVGDLVFAIGNPFGVGESVTQGIVSALNKSG--IGI-NSYENF 121
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                IQTDASINPGNSGGALIDSRGGLVGINTAIISKTGGNHGIGFAIPSNMVKDTVTQL---- 177
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             IKTGKIERGYLGVGLQDLSGDLQNSY-----DNKEGAVVISVEKDSPAKKAGILVWD 229
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   12 GSGVIISKDGYIVTNNHVID-----GADKIKVTIPGSNKEYSATLVGTDSESDLAVIRI 65
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      33;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               18.3%; Score 355.5; DB 10; Length 286; 33.1%; Pred. No. 4.1e-20;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               FILE REFERENCE: 19201
CURRENT APPLICATION NUMBER: US/09/764,898
CURRENT FILING DATE: 201-01-17
Prior application data removed - consult PALM or file wrapper NUMBER OF SEQ 1D NOS: 311
SOFTWARE: PatentIn Ver. 2.0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Sequence 256, Application US/09764898
Patent No. US20020090673A1
GENERAL INFORMATION:
APPLICANT: Rosen et al.
TITLE OF INVENTION: Nucleic Acids, Proteins, and Antibodies
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           LITEVNGKKVKNTNELRNLIGSMLPNORVTLKVIRDKKERAFTL 273
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           95;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        62; Mismatches
                                                                                                                                                                                                                                                                                                                                                                         LITEVNGKKVKNTNELRNLIGSMLPNQRVTL 260
```

g

```
Query Match
Best Local Similarity
Matches 70; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    NAME/KEY: SITE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                       NAME/KEY: SITE
                                                                                                     US-09-764-898-184
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               US-09-764-898-184
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               US-09-712-363-161
                                                                                                                                                                                                                                                                                                                                                                                                       TYPE: PRT
                                                                                                                                                                                                                                                                                                                                                                                                                                                 FEATURE:
                                                                                                                                                                                                                                                                                                                                                                                     LENGTH:
                        g
G
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  qq
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ð
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        QQ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       g
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  à
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          10;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        202 GSGFIVSEDGLIITNAHVVRNQQWIEVVLQ-NGARYEAVVDIDLKLDLAVIKIESNAEL 260
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               128 INPGNSGGALIDSRGGLVGINTAIISKTGGNHGIGFAIPSNMVKDTVTQLIK---TGKI- 183
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                71 PTIKFSDSNDISVGDLVFAIGNPFGVGESVTQGIVSALNKSG--IGI-NSYENFIQTDAS 127
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        184 -ERGYLGVGLQD----LSGDLQNSY----DNKEGAVVISVEKDSPAKKAGILVWDLITEV 234
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             12 GSGVIISKDGYIVTNNHVIDGADKIKVTIPGSNKEYSATLVGTDSESDLAVIRITKD-NL 70
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        27;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Length 476;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     17.6%; Score 3*0....31.9%; Pred. No. 1.1e-18; stive 61; Mismatches 102; Indels ...ive 61; Mismatches 102; Indels ...ive
240 IIVKVNGRPLVDSSELQE --- AVLTESPLLLEVRRGNDDLLFSI 280
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        COMPUTER: IBM Compatible
OPERATIOS SYSTEM: DOS
SOFTWARE: FastSEQ for Windows Version 2.0
CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         235 NGKKVKNTNELRNLIGSMLPNQRVTLKVIRDKKERAFTL 273
                                                                                                                                                                                                                                  Williams, Lewis T.
Kothakota, Srinivas
TITLE OF INVENTION: Secreted Human Proteins
NUMBER OF SEQUENCES: 38
CORRESPONDENCE ADDRESS:
ADDRESSEE: Chiron Corporation
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           APPLICATION NUMBER: US/09/935,390A FILING DATE: 22-Aug-2001 CLASSIFICATION: <Unknown>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            NAME: Jane E. R. Potter
REGISTRATION NUMBER: 33,332
REFERENCE/DOCKET NUMBER: 1369.002
TELECOMMUNICATION INFORMATION:
TELEPHONE: (510) 923-2718
TELEFAX: (510) 655-3542
TELEFAX: (510) 655-3542
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       TOPOLOGY: linear
MOLECULE TYPE: No. US20020076761Ale
SEQUENCE DESCRIPTION: SEQ ID NO: 37.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           PRIOR APPLICATION DATA: APPLICATION NUMBER: 08/988,671
                                                                                                                                                                                                                                                                                                                                                           STREET: 4560 Horton Street
                                                                                                     Sequence 37, Application US/09935390A Patent No. US20020076761A1 GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     FILING DATE: 1997-12-11
ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           LENGTH: 476 amino acids
                                                                                                                                                                                                                                                                                                                                                                                                                      COUNTRY: USA
ZIP: 94608-2916
COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette
                                                                                                                                                                  APPLICANT: Escobedo, Jaime Quianjin, Hu
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           TYPE: amino acid
STRANDEDNESS: single
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             INFORMATION FOR SEQ ID NO: 37: SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                              Garcia, Pablo
                                                                                                                                                                                                                                                                                                                                                                                   CITY: Emeryville
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Query Match
Best Local Similarity 31.9°
Matches 89; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  US-09-935-390A-37
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             261
```

d Q

ò

q ò g à g à

```
LOCATION: (265)
OTHER INFORMATION: Xaa equals any of the naturally occurring L-amino acids
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              GEMERAL INFORMATION:

APPLICANT: Elsenberg, David

APPLICANT: Elsenberg, David

APPLICANT: Elsenberg, David

APPLICANT: Elsenberg, David

TITLE OF INVENTION: DETERMINING THE FUNCTIONS AND

TITLE OF INVENTION: DETERMINING THE FUNCTIONS AND

TITLE OF INVENTION: DETERMINING THE FUNCTIONS OF PROTEINS BY COMPARATIVE ANALYSIS

FILE REFERENCE: 074,9-03201

CURRENT APPLICATION NUMBER: US/09/712,363

CURRENT PELLING DATE: 2000-01-13

PRIOR FILING DATE: 3000-01-28

PRIOR PELLING DATE: 3000-02-01

PRIOR PELLING DATE: 3099-02-01

PRIOR PELLING DATE: 3999-02-01

PRIOR FILING DATE: 3999-02-01

PRIOR FILING DATE: 3999-05-14

PRIOR FILING DATE: 3999-05-14

PRIOR FILING DATE: 3999-05-14

PRIOR FILING DATE: 3999-05-14
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           LOCATION: (244)
OTHER INFORMATION: Xaa equals any of the naturally occurring L-amino acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    66 -TKDNLPTIKFSUSNDISVGDLVFAIGNPFGVGESVTQGIVSALNKSG--IGI-NSYENF 121
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 207 HPKKKLPVLLLGHSADLRPGEFVVAIGSPFALQNTVTXGIVSTAQREGRELGLRDSDMXY 266
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 12 GSGVIISKDGYIVTNNHVID-----GADKIKVTIPGSNKEYSATLVGTDSESDLAVIRI 65
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               122 IQTDASINPGNSGGALIDSRGGLVGINTAIISKTGGNHGIGFAIPSNMVKDTVTQ 176
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      16;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Length 330;
                                                                                                                                                                                                                                                                                                                                                                                                                       - consult PALM or file wrapper
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          14.9%; Score 289; DB 10;
40.0%; Pred. No. 5.7e-15;
tive 33; Mismatches 56;
APPLICANT: Rosen et al.
TITLE OF INVENTION: Nucleic Acids, Proteins, and
FILE REFERENCE: PJZ01
CURRENT APPLICATION NUMBER: US/09/764,898
CURRENT FILING DATE: 2001-01-17
Prior application data removed - consult PALM or
NUMBER OF SEQ ID NOS: 311
SOFTWARE: Patentin Ver. 2.0
SEQ ID NO 184
                                                                                                                                                                      Sequence 184, Application US/09764898
Patent No. US20020096673A1
GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Sequence 161, Application US/09712363 Patent No. US20020164588A1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ORGANISM: Homo sapiens
```

```
RESULT 14
US-09-712-363-280
                                                                                                                                                                                                                                                                                                                                                122
                                                                                                                                                                                   엄
                                                                                                                                                                                                                                           à
                                                                                                                                                                                                                                                                                          g
                                                                                                                                                                                                                                                                                                                                                ò
                                                                                                                                                                                                                                                                                                                                                                                         qq
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 g
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ò
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   a
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            õ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ò
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                APPLICANT: Alderson, Mark
APPLICANT: Campos-Neto, Antonio
APPLICANT: Campos-Neto, Antonio
APPLICANT: Campos-Neto, Antonio
APPLICANT: Campos-Neto, Antonio
TITLE OF INVENTION: Evision Protiens of Mycobacterium tuberculosis Antigens
TITLE OF INVENTION: and Their Uses
CURRENT APPLICATION NUMBER: US/09/287,849
CURRENT FILING DATE: 1999-04-07
PRIOR PAPLICATION NUMBER: US 08/818,112
PRIOR PAPLICATION NUMBER: US 08/942,578
PRIOR APPLICATION NUMBER: US 09/025,197
PRIOR APPLICATION NUMBER: US 09/025,197
PRIOR PLING DATE: 1998-02-18
PRIOR PLING DATE: 1998-02-18
PRIOR FILING DATE: 1998-02-18
PRIOR FILING DATE: 1998-03-18
PRIOR FILING DATE: 1998-04-07
PRIOR APPLICATION NUMBER: US 09/025,3040
PRIOR FILING DATE: 1998-03-18
PRIOR FILING DATE: 1998-03-18
PRIOR FILING DATE: 1998-03-18
PRIOR APPLICATION NUMBER: US 09/023,040
PRIOR FILING DATE: 1998-03-18
PRIOR ELING DATE: 1998-03-18
PRIOR APPLICATION NUMBER: US 09/023,040
                                                                                                                                                                                                                                                                                                                                                                                                   10;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  139 PSAAI -- GGGVAVGEPVVAMGNSGGGGTPRAVPGRVVALGOTVQASDSLTGAEETLNGL 196
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         71 PTIKFSDSNDISVGDLVFAIGNPFGVGES--VTQGIVSALNKSGIGINS-----YENF 121
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                122 IQTDASINPGNSGGALIDSRGCLVGINTAIIS----KTGGNHGIGFAIPSNMVKDTVTQL 177
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ----YLGVGLQDLSGDLQNSYDNKEGAVVISVEKDSPAKKAGI 225
                                                                                                                                                                                                                                                                                                                                                                                                                                                    12 GSGVIISKDGYIVTNNHVIDGADKIKVTIPGSNKEYSATLVGTDSESDLAVIRIT-KDNL 70
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             248 AIAGQIRSGGGSPTVHIGPTAFLGLGVVD------NNGNGARVQRVVGSAPAASLGI
                                                                                                                                                                                                                                                                                                                                                                                                   47;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        226 LVWDLITEVNGKKVKNTNELRNLIGSMLPNORVTLK-VIRDKKERAFTLTLAE 277
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      299 STGDVITAVDGAPINSATAMADALNGHHPGDVISVTWQTKSGGTRTGNVTLAE 351
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ; OTHER INFORMATION: Description of Artificial Sequence:bi-fusion US-09-287-849-26
                                                                                                                                                                                                                                                                                                                                                Length 355;
                                                                                                                                                                                                                                                                                                                                                                                                   Indels
                                                                                                                                                                                                                                                                                                                                                                                                 47; Mismatches 112;
                                                                                                                                                                                                                                                                                                                                             14.5%; Score 281.5; DB 9; 29.7%; Pred. No. 2.3e-14;
PRIOR FILING DATE: 1999-05-14
PRIOR APPLICATION NUMBER: 60/165,124
PRIOR FILING DATE: 1999-11-12
PRIOR PLICATION NUMBER: 60/165,086
PRIOR APPLICATION NUMBER: 60/165,086
PRIOR FILING DATE: 1999-11-12
NUMBER OF SEQ ID NOS: 292
SOFTWARE: FastSEQ for Windows Version 4.0
SEQ ID NO 161
LENGTH: 355
                                                                                                                                                                                                                                      TYPE: PRT : ORGANISM: Mycobacterium tuberculòsis US-09-712-363-161
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           US-09-287-849-26
; Sequence 26, Application US/09287849
; Patent No. US20020009459A1
; GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               APPLICANT: Reed, Steven G. APPLICANT: Skeiky, Yasir A.W. APPLICANT: Dillon, Davin C.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ORGANISM: Artificial Sequence
                                                                                                                                                                                                                                                                                                                                                                      Best Local Similarity 29.78
Matches 87; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   APPLICANT:
APPLICANT:
APPLICANT:
                                                                                                                                                                                                                                                                                                                                                Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ò
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       g
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           a
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     a
                                                                                                                                                                                                                                                                                                                                                                                                                                                       ò
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             à
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ò
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ò
```

```
APPLICANT: DILLOW, MAIN C.
APPLICANT: Campos-Neto, Antonio
APPLICANT: Campos-Neto, Antonio
APPLICANT: Campos-Neto, Antonio
APPLICANT: Corixa Corporation
TITLE OF INVENTION: Fusion Protiens of Mycobacterium tuberculosis Antigens
TITLE OF INVENTION: and Their Uses
TITLE OF INVENTION: and Their Uses
TITLE OF INVENTION: and Their Uses
FILE REFERENCE: 014058-009020uS
CURRENT APPLICATION NUMBER: US 08/818,112
PRIOR FILING DATE: 1999-04-07
PRIOR FILING DATE: 1997-10-01
PRIOR FILING DATE: 1998-02-18
PRIOR FILING DATE: 1998-04-07
PRIOR FILING DATE: 1998-04-07
PRIOR FILING DATE: 1998-04-07
PRIOR APPLICATION NUMBER: US 09/223,040
PRIOR FILING DATE: 1998-12-30
NUMBER OF SEQ ID NOS: 46
SEQ ID NO 2
LENTH: 729
                                                    ..
..
                                                                                                                                PTIKESDSNDISVGDLVFAIGNPFGVGES--VTQGIVSALNKSGIGINS-----YENF 121
                                                                                                                                                                                                                                  71 PTIKFSDSNDISVGDLVFAIGNPFGVGES--VTQGIVSALNKSGIGINS-----YENF 121
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Gaps
                                                                                                    12 GSGVIISKDGYIVTNNHVIDGADKIKVTIPGSNKEYSATLVGTDSESDLAVIRIT-KDNL 70
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     12 GSGVIISKDGYIVTNNHVIDGADKIKVTIPGSNKEYSATLVGTDSESDLAVIRIT-KDNL 70
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  FEATURE: COTHER INFORMATION: Description of Artificial Sequence:tri-fusion US-09-287-849-2
Length 596;
                                                  Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Query Match 10.9%; Score 211; DB 10; Best Local Similarity 35.6%; Pred. No. 1.5e-08; Matches 53; Conservative 28; Mismatches 56;
Score 211; DB 10;
Pred. No. 1.1e-08;
Query Match 10.9%; Score 211; DB Best Local Similarity 35.6%; Pred. No. 1.1e Matches 53; Conservative 28; Mismatches
                                                                                                                                                                                                                                                                                                         IQTDASINPGNSGGALIDSRGGLVGINTA 150
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        122 IQTDASINPGNSGGALIDSRGGLVGINTA 150
                                                                                                                                                                                                                                                                                                                                   Sequence 2, Application US/09287849
Patent No. US20020009459A1
GENERAL INFORMATION:
APPLICANT: Reed, Steven G.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   TYPE: PRT ORGANISM: Artificial Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           APPLICANT: Reed, Steven G. APPLICANT: Skeiky, Yasir A.W. APPLICANT: Dillon, Davin C.
```

```
ä
                                                                                                            APPLICANT: Elsenbergy, Lawlud
APPLICANT: Elsenbergy, Lawlud
APPLICANT: Ascrete, Edward M.
APPLICANT: Marcotte, Edward M.
TITLE OF INVENTION: DETREMAINED THE FUNCTIONS AND
TITLE OF INVENTION: DETREMAINED OF PROTEINS BY COMPARATIVE ANALYSIS
TITLE OF INVENTION: LIWERACTIONS OF PROTEINS BY COMPARATIVE ANALYSIS
TITLE APPLICATION NUMBER: US/09/712,363
CURRENT APPLICATION NUMBER: BOT-10-13
PRIOR FILING DATE: 2000-10-12
PRIOR FILING DATE: 1990-02-01
PRIOR FILING DATE: 1990-02-01
PRIOR PILING DATE: 1990-02-01
PRIOR FILING DATE: 1990-02-04
PRIOR FILING DATE: 1990-02-05-14
PRIOR PLILING DATE: 1990-05-14
PRIOR PLILING DATE: 1990-05-14
PRIOR PLILING DATE: 1990-05-14
PRIOR PLILING DATE: 1990-05-14
PRIOR PLILING DATE: 1990-01-12
PRIOR PLILING DATE: 1990-01-12
PRIOR PLILING DATE: 1990-01-12
PRIOR PLILING DATE: 1990-01-11-12
PRIOR PLILING DATE: 1990-01-11-12
PRIOR PLILING DATE: 1990-01-11-12
PRIOR PLILING DATE: 1990-01-11-12
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         65 ITKDNLPTIKFSDSNDISVGDLVFAIGNPFGVGESVTQG-IVSALNKSGIGINSYENFIQ 123
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      270 VPHLPPPPLVFA-AEPAKTGADVVVLGYPGGGNFTATPARIREAIRLSGPDIYGDPEPVT 328
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   124 TD-----ASINPGNSGGALIDSRGCLVGI------NTAIISKTGGNHGIGFAIPSNM 169
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       6 RMERAL-GSGVIISKDGYIVTNNHVIDGADKIKVTIPGSNKEYSATLVGTDSESDLAVIR 64
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Sequence 1, Application US/09841786
Batent No. US20020054883A1
GENERAL INFORMATION:
APPLICANT: NAGARAJA, T. G.
APPLICANT: STEWART, GEORGE C.
APPLICANT: CHENGAPPA, M. M.
APPLICANT: CHENGAPPA, M. M.
TITLE OF INVENTION: RECOMBINANT FUSOBACTERIUM NECROPHORUM LEUKOTOXIN
TITLE OF INVENTION: VACCINE AND PREPARATION THEREOF
FILE REFERENCE: 30296
CURRENT APPLICATION NUMBER: US/09/841,786
CURRENT FILING DATE: 2001-04-24
PRIOR APPLICATION NUMBER: 09/558,257
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Length 397;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Query Match 7.6%; Score 147.5; DB 9; Best Local Similarity 27.1%; Pred. No. 0.00043; Matches 52; Conservative 33; Mismatches 80;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    NUMBER OF SEQ ID NOS: 292
SOFTWARE: FastSEQ for Windows Version
SEQ ID NO 280
Sequence 280, Application US/09712363
Patent No. US20020164588A1
GENERAL INFORMATION:
APPLICANT: Elsenberg, David
APPLICANT: Rotstein, Sergio H.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Mycobacterium tuberculosis
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                170 VKDTVTQLIKTG 181
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         US-09-712-363-280
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  US-09-841-786-1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            g
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ŏ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            g
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       οy
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               g
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ŏ
```

```
22;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  : ::: | ::| ::| 121 | 1822 | 1825 | 1822 | 1822 | 1822 | 1823 | 1823 | 1823 | 1823 | 1823 | 1823 | 1823 | 1823 | 1823 | 1823 | 1823 | 1823 | 1823 | 1823 | 1823 | 1823 | 1823 | 1823 | 1823 | 1823 | 1823 | 1823 | 1823 | 1823 | 1823 | 1823 | 1823 | 1823 | 1823 | 1823 | 1823 | 1823 | 1823 | 1823 | 1823 | 1823 | 1823 | 1823 | 1823 | 1823 | 1823 | 1823 | 1823 | 1823 | 1823 | 1823 | 1823 | 1823 | 1823 | 1823 | 1823 | 1823 | 1823 | 1823 | 1823 | 1823 | 1823 | 1823 | 1823 | 1823 | 1823 | 1823 | 1823 | 1823 | 1823 | 1823 | 1823 | 1823 | 1823 | 1823 | 1823 | 1823 | 1823 | 1823 | 1823 | 1823 | 1823 | 1823 | 1823 | 1823 | 1823 | 1823 | 1823 | 1823 | 1823 | 1823 | 1823 | 1823 | 1823 | 1823 | 1823 | 1823 | 1823 | 1823 | 1823 | 1823 | 1823 | 1823 | 1823 | 1823 | 1823 | 1823 | 1823 | 1823 | 1823 | 1823 | 1823 | 1823 | 1823 | 1823 | 1823 | 1823 | 1823 | 1823 | 1823 | 1823 | 1823 | 1823 | 1823 | 1823 | 1823 | 1823 | 1823 | 1823 | 1823 | 1823 | 1823 | 1823 | 1823 | 1823 | 1823 | 1823 | 1823 | 1823 | 1823 | 1823 | 1823 | 1823 | 1823 | 1823 | 1823 | 1823 | 1823 | 1823 | 1823 | 1823 | 1823 | 1823 | 1823 | 1823 | 1823 | 1823 | 1823 | 1823 | 1823 | 1823 | 1823 | 1823 | 1823 | 1823 | 1823 | 1823 | 1823 | 1823 | 1823 | 1823 | 1823 | 1823 | 1823 | 1823 | 1823 | 1823 | 1823 | 1823 | 1823 | 1823 | 1823 | 1823 | 1823 | 1823 | 1823 | 1823 | 1823 | 1823 | 1823 | 1823 | 1823 | 1823 | 1823 | 1823 | 1823 | 1823 | 1823 | 1823 | 1823 | 1823 | 1823 | 1823 | 1823 | 1823 | 1823 | 1823 | 1823 | 1823 | 1823 | 1823 | 1823 | 1823 | 1823 | 1823 | 1823 | 1823 | 1823 | 1823 | 1823 | 1823 | 1823 | 1823 | 1823 | 1823 | 1823 | 1823 | 1823 | 1823 | 1823 | 1823 | 1823 | 1823 | 1823 | 1823 | 1823 | 1823 | 1823 | 1823 | 1823 | 1823 | 1823 | 1823 | 1823 | 1823 | 1823 | 1823 | 1823 | 1823 | 1823 | 1823 | 1823 | 1823 | 1823 | 1823 | 1823 | 1823 | 1823 | 1823 | 1823 | 1823 | 1823 | 1823 | 1823 | 1823 | 1823 | 1823 | 1823 | 1823 | 1823 | 1823 | 1823 | 1823 | 1823 | 1823 | 1823 | 1823 | 1823 | 1823 | 1823 | 1823 | 1823 | 1823 | 1823 | 1823 | 1823 | 1823 | 1823 | 1823 | 1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        1823 KTVSSHVDQTDII)KDLEEENNGNKEKANVNVLAENTSQVVTNATVLSGASGQAAVGAGVA 1882
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              1501 KEQLEKAK-----KKEGAVIVNAALSVAGTDKSAGGVAIAVNTVKNKFKAELSGSNKEA 1554
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         1555 GEDKIHAKHVNVEAKSSTVVVNAASGLAISKDAFSGMGSGAWQDLSNDTIAKVDKGRISA 1614
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           .673 KVNVQALNDSHIJINVSAGGAASİKQA------GIGGMVSVNRGSDETEALVSDSEFE 1723
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        84 GDLVFAIGNPFGVGESVTQGLVSALNKSGIG-----INSYENFIQTDASINPGNSGGA 136
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       137 LID------SRGGLVGINTAIISKTGGNHGIGFAIPSNMVKDTVTQLIKTGKIE 184
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ------GAQGQL---NGLQ 301
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        VEDLIQETKRSMKLS-DDVQGVLVSQVNENS-----PAEQAGFRQGNIITKIEEV 350
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      185 RGYLGVGLQDLSGDLQNSYDNKEGAVVISVEKDSPAKKAGILVWDLITEVNGKKVKNTNE 244
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               47 ----YSATLVGTCSESDLAVIR-----ITKD-------NLPTIKFSDSNDISV 83
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ---KIKVTIPGSNKE- 46
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    1615 DSLNVNANNSI-IGVNVAGTIAGSLS-TAVGAAFANNTLHNKTSALITGTKVNPFSGKNT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Query Match 7.2%; Score 139; DB 10; Length 3241;
Best Local Similarity 19.9%; Pred. No. 0.034;
Matches 99; Conservative 68; Mismatches 156; Indels 174;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                4 KERMERALGSGVIISKDGYIVTNNHV-IDGAD----
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Search completed: November 18, 2002, 11:33:41
Job time: 14 secs
                                                                                                                                                                                                                                                                                                                            ORGANISM: Fusobacterium necrophorum US-09-841-786-1
PRIOR FILING DATE: 2000-04-25
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          1942 -- NTIAELNHAKETAKG 1956
                                         NUMBER OF SEQ ID NOS: 15
SOFTWARE: Patentin Ver.
SEQ ID NO 1
                                                                                                                                                                                                                   LENGTH: 3241
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               g
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         g
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  g
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     g
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               δ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        οy
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  g
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ŏ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           d
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ŏ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          qq
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ò
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   셤
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ò
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ò
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ò
```

0	٠.
\	
-1	
.)	
K	
7	•
6)
_	
	4
rai	,
ra	
•	
N	
0	
~	
-	
ď	
m	
91	
- 1	
95	
89	
1	
60	
ns.	
3	

```
Appli
Appli
                                           Appli
                                                                                                             Appli
Appli
Appli
Appli
                                                                                                                                                  Appli
Appli
Appli
                                                                   Appl
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ALGSGVIISKD-(;YIVTNNHVIDGADKIKVTIPGSNKEYSATLVGTDSESDLAVIRI-TK 67
                Sequence
Sequence
Sequence
Sequence
Sequence
                                                                                 Sequence
Sequence
                                                                                                           Sequence
Sequence
Sequence
                                                                                                                                                 Sequence
Sequence
Sequence
Sequence
Sequence
                                                                                                                                                                                                                                  Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         25;
                                                                                                                                                                                                                                                                                                                                                                                                                                                    of Haemophilus Hin47 Protein with
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Length 472;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    SOFTWARE: Patentin Release #1.0, Version #1.25 CURRENT APPLICATION DATA: APPLICATION NUMBER: US/08/278,091 FILING DATE: 21-JUL-1994 CLASSIFICATION: 435 ATTORNEY/AGENT INFORMATION:
US-08-350-741-2
US-08-463-875A-2
US-08-350-741-3
US-08-199-637A-132
US-08-480-593-2
US-08-480-593-2
US-08-280-2
US-08-280-2
US-08-472-173-2
US-08-472-173-2
US-08-472-173-2
US-08-472-173-2
US-08-472-173-2
US-08-482-816-2
                                                                                                                                                                                                                                                                                                                                                                                                                                                  TITLE OF INVENTION: Analog of Haemophilus Hin-
TITLE OF INVENTION: Reduced Protease Activity
WIMBER OF SEQUENCES: 23
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              .4e-53
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         5: Sim & McBurney
Suite 701, 330 University Avenue
                                                                                                                                                                                       US-08-801-499-2
US-08-615-271-2
US-09-074-660-2
US-09-074-659-2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Score 725.5;
Pred. No. 1.4
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              TORNEY Abena .... Michael I NAME: Stewart, Michael I REGISTRATION UNMBER: 24,973
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   COMPUTER READBLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  37.4%; Scc...
43.2%; Pred
75;
                                                                                                                                                                                                                                                                                                                                        Sequence 5, Application US/08278091
Patent No. 5506139
GENERAL INFORMATION:
APPLICANT: LOOSNORE, Sheena M
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 REFERENCE/DOCKET NUMBER: 1(TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                               APPLICANT: LOOSNORE, Sheena PAPLICANT: YANG, Yan-Ping APPLICANT: CHONG, Pele APPLICANT: OOMEN, RAYMOND P. APPLICANT: KLEIN, Michel H.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          TELEPHONE: (415) 595-1155
TELEFAX: (416) 595-1163
INFORMATION FOR SEQ ID NO: 5:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    LENGTH: 472 amino acids
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     SEQUENCE CHARACTERISTICS:
                           single
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          linear
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           COUNTRY: Canada
ZIP: M5G 1R7
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  STREET: Suite 7 CITY: Toronto STATE: Ontario
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Ontario
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           STRANDEDNESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ADDRESSEE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          TOPOLOGY:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Query Match
Best Local Simi
Matches 163;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     US-08-278-091-5
                                                                                                                                                                                                                                                                                                                           US-08-278-091-5
                           714.5
714.5
706.5
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     10
    44440933644444493994444493944444939444449394444
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ò
                                                                                                             (without alignments)
632.593 Million cell updates/sec
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    is the number of results predicted by chance to have a neer than or equal to the score of the result being printed, ived by analysis of the total score distribution.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Sequence 5,                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Description
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Sequence 6
Sequence 6
Sequence 6
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Sequence S
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Sequence
                                                                                                                                                             1938
1 MIPKERMERALGSGVIISKD.......KPKRFLVLDLNQGYRIILVK
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Sequence.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Seguence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Sequence
                                                                                          November 18, 2002, 11:28:15 ; Search time 18 Seconds
                                                                                                                                                                                                                                                                                                                                                                                                        /cgn2_6/ptodata/1/iaa/5A_COMB.pep:*
/cgn2_6/ptodata/1/iaa/5B_COMB.pep:*
/cgn2_6/ptodata/1/iaa/6A_COMB.pep:*
/cgn2_6/ptodata/1/iaa/6B_COMB.pep:*
/cgn2_6/ptodata/1/iaa/PCTUS_COMB.pep:*
/cgn2_6/ptodata/1/iaa/PCTUS_COMB.pep:*
               GenCore version 5.1.3
Copyright (c) 1993 - 2002 Compugen Ltd
                                                                                                                                                                                                                                                                   Total number of hits satisfying chosen parameters:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                US-08-923-454A-14
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    US-09-074-660-5
US-09-074-659-5
US-09-106-468-5
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      US-08-615-271-5
                                                                                                                                                                                                                                            262574 seqs, 29422922 residues
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           SUMMARIES
                                                                                                                                                                                                                                                                                                                                     Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries
                                                                   protein search, using sw model
                                                                                                                                                                                                     BLOSUM62
Gapop 10.0 , Gapext 0.5
                                                                                                                                                                                                                                                                                                                                                                                             Issued_Patents_AA:*
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  score greater than or equal to
and is derived by analysis of
                                                                                                                                                 US-09-895-913A-120
                                                                                                                                                                                                                                                                                                 length: 0
length: 2000000000
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  DB
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Length
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Query
                                                                                                                                                                                                                                                                                                                                                                                                            ........
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Pred. No.
                                                                                                                                                                                                                                                                                              Minimum DB seq
Maximum DB seq
                                                                                                                                               Title:
Perfect score:
                                                                                                                                                                                                      coring table:
                                                                   OM protein
                                                                                                                                                                                                                                            Searched:
                                                                                                                                                                           Sequence:
                                                                                                                                                                                                                                                                                                                                                                                              Database
                                                                                            Run on:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      tesult
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             17
118
119
22
23
24
25
26
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Ş
```

ó

us-09-895-913a-120_2.rai

```
112 ALGSGVIIDADKGYVVTNNHVVDNATVIKVQL-SDGRKFDAKMVGKDPRSDIALIQIQNP 170
                                                                                                                                                                                                                    188 LGVGLODLSGDLQNS--YDNKEGAVVISVEKDSPAKKAGILVWDLITEVNGKKVKNTNEL 245
                                                                                                                                                                                                                                                                                                    246 RNLIGSMLPNQRVTLKVIRDKKERAFTLTLAERKNPNKKETISAQNGAQGQLNGLQVEDL 305
                                                                                                                                                                                                                                                                                                                                                                                         306 TQETKRSMRLSDDVQGVLVSQVNENSPAEQAGFRQGNIITKIEEVEVKSVADFNHALEKY 365
                                                                                                                                                                                                                                                                                                                                                                                                             68 DNLPTIKFSDSNDISVGDLVFAIGNPFGVGESVTQGIVSALNKSGIGINSYENFIQTDAS 127
                                                                                                                               128 INPGNSGALIDSRGGLVGINTAIISKTGGNHGIGFAIPSNMVKDTVTQLIKTGKIERGY 187
                                                                                                                                                                                                                                                                                                                               Sequence 5, Application US/08483859
Patent NO. 5656436
GENERAL INFORMATION:
APPLICANT: LOOSMORE, Sheena M.
APPLICANT: YanG, Yan-Ping
APPLICANT: COMBO, Pele
APPLICANT: COMBO, Pele
APPLICANT: KLEIN, Michel H.
TITLE OF INVENTION: Analog of Haemophilus Hin47 Protein with
TITLE OF INVENTION: Reduced Protease Activity
NUMBER OF SEQUENCES: 23
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Version #1.25
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      E: Sim & McBurney
Suite 701, 330 University Avenue
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               1038-495 MIS:VQ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/296,149
FILING DATE: 26-AUG-1994
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/278,091
FILING DATE: 21-JUL-1994
ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPPRATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PATENTIN Release #1.0.
CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                APPLICATION NUMBER: US/08/483,859
FILING DATE: 07-JUN-1995
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                NAME: Stewart, Michael I.
REGISTRATION NUMBER: 24,973-
REFERENCE/DOCKET NUMBER: 1038-
TELECOMMUNICATION INFORMATION:
TELEPAN: (416) 595-1155
TELEPAN: (416) 595-1163
INFORMATION FOR SEC ID NO: 5:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                           366 KGKPKRFLVLDLNQGYR 382
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      453 -SKPS-VLALNIQRGDR 467
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            472 amino acids
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                amino acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        STREET: Suite 7C
CITY: Toronto
STATE: Ontario
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                COUNTRY: Canada
ZIP: M5G 1R7
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ADDRESSEE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  RESULT 2
US-08-483-859-5
                                                                                                                                                                     g
                                                                                                                                                                                                                                                          g
                                                                                                                                                                                                                                                                                                  ò
                                                                                                                                                                                                                                                                                                                                            g
                                                                                                                             õ
                                                                                                                                                                                                                 å
                                                                                                                                                                                                                                                                                                                                                                                         ô
```

```
9
                                                                                                                                                                                                                                                                                    231 INRGNSGGALVNLNGELIGINTAILAPDGGNIGIGFAIPSNMVKNLTSQMVEYGQVKRGE 290
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        306 TQETKRSMRLSDDVQGVLVSQVNENSPAEQAGFRQGNIITKIEEVEVKSVADFNHALEKY 365
                                                                                                                                                                                                                                                             DNLPTIKFSDSNDISVGDLVFAIGNPFGVGESVTQGIVSALNKSGIGINSYENFIQTDAS 127
                                                                                                                                                                                                                                                                                                                                                   128 INPGNSGALIDSRGGLVGINTAIISKTGGNHGIGFAIPSNMVKDTVTQLIKTGKIERGY 187
                                                                                                                                                                       10 ALGSGVIISKD-GYIVTNNHVIDGADKIKVTIPGSNKEYSATLVGTDSESDLAVIRI-TK 67
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           RNLIGSMLPNQRVTLKVIRDKKERAFTLTLAERKNPNKKETISAQNGAQGQLNGLQVEDL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    LGVGLQDLSGDLQNS--YDNKEGAVVISVEKDSPAKKAGILVWDLITEVNGKKVKNTNEL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              TITLE OF INVENTION: Analog of Haemophilus Hin47 Protein with TITLE OF INVENTION: Reduced Protease Activity
                                                                                      Length 472;
                                                                                                                            Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    SOFTWARE: Patentin Release #1.0, Version #1.25 CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/472,173 FILING DATE: 07-JUN-1995 CLASSIFICATION: 435
                                                                                 Query Match 37.4%; Score 725.5; DB 1; Best Local Similarity 43.2%; Pred. No. 1.4e-53; Matches 163; Conservative 75; Mismatches 114;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ADDRESSEE: Sim & McBurney
STREET: Suite 701, 330 University Avenue
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      CLASSIFICATION: 435

CLASSIFICATION: 435

PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/296,149

FILING DATE: 26-NG-1994

PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/278,091

FILING DATE: 21-JUL-1994

ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Sequence 5, Application US/08472173
Patent No. 5665353
GENERAL INFORMATION:
APPLICANT: LOOSMORE, Sheena M
APPLICANT: YANG, Yan-Ping
APPLICANT: CHONG, Pele
APPLICANT: CHONG, RAYMOND PELICANT: CHONG, RAYMOND PELICANT: CHONG, RAYMOND PELICANT: CHONG, RAYMOND PELICANT: KLEIN, Michel H.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     366 KGKPKRFLVLDLNQGYR 382
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              NUMBER OF SEQUENCES: 23
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             CITY: Toronto
STATE: Ontario
COUNTY: Canada
ZIP: MSG 1R7
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy di
  single
                      ; TOPOLOGY: linear
US-08-483-859-5
STRANDEDNESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               US-08-472-173-5
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           246
                                                                                                                                                                                                                                                             68
                                                                                                                                                                                                                                                                                                                                                                                                                                       188
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          400
                                                                                                                                                                                                                                                                                                                                                                                                                                                                              g
                                                                                                                                                                                                                                                                ò
                                                                                                                                                                                                                                                                                                      g
                                                                                                                                                                                                                                                                                                                                                                                          a
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ŏ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    g
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        g
                                                                                                                                                                                                                                                                                                                                                   ò
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ò
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ò
```

```
246 RNLIGSMLPNQRVTLKVIRDKKERAFTLTLAERKNPNKKETISAQNGAQGQLNGLQVEDL 305
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            68 DNLPTIKFSDSNDISVGDLVFAIGNPFGVGESVTQGIVSALNKSGIGINSYENFIQTDAS 127
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      128 INPGNSGGALIFSRGGLVGINTAIISKTGGNHGIGFAIPSNMVKDTVTQLIKTGKIERGY 187
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           10 ALGSGVIISKD.GYIVTNNHVIDGADKIKVTIPGSNKEYSATLVGTDSESDLAVIRI-TK 67
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             LGVGLQDLSGDLQNS--YDNKEGAVVISVEKDSPAKKAGILVWDLITEVNGKKVKNTNEL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          306 TQETKRSMRLSDOVQGVLVSQVNENSPAEQAGFRQGNIITKIEEVEVKSVADFNHALEKY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         25;
                                                                                                                                                                                                                                                                                                                                                                                                                                       Length 472;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                    Query Match 37.4%; Score 725.5; DB 2; Best Local Similarity 43.2%; Pred. No. 1.4e-53; Matches 163; Conservative 75; Mismatches 114;
                                                                                                                                                                                                                   1038-508 MIS:vg
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            E: Sim & McBurney
Suite 701, 330 University Avenue
                                              PRIOR APPLICATION 473.

PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/296,149
FILING DATE: 26-AGG-1994
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/278,091
FILING DATE: 21-UUL-1994
ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           APPLICANT: LOOSMURE, Sheena M
APPLICANT: YANG, Yan-Ping
APPLICANT: CHONG, Pele
APPLICANT: OOMEN, Raymond P.
APPLICANT: KLEIN, Michel H.
TITLE OF INVENTION: Analog of Ha
                                                                                                                                                                              NAME: Stewart, Michael I.
REGIGTRATION NIMBER: 24,973
REFERENCE/COCKT NUMBER: 1038
TELECOMMUNICATION INFORMATION:
TELEPHONE: (416) 595-1155
INFORMATION FOR SEQ ID 00: 5: SEQUENCE CHARACTERISTICS:
LENGTH: 472 amino acids
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Sequence 5, Application US/08482816
Patent No. 5935573
GENERAL INFORMATION
             07-JUN-1995
: 435
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   453 -SKPS-VLALNIORGDR 467
                                                                                                                                                                                                                                                                                                                                             ; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
US-08-487-167-5
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           CORRESPONDENCE ADURESS:
ADDRESSEE: Sim & MCB
 APPLICATION NUMBER:
                                 CLASSIFICATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ADDAL.
STREET: Surr.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          US-08-482-816-5
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         RESULT 5
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             g
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       d
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  δ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    g
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           q
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ò
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    g
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    δ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ŏ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               g
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ò
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               δ
                                                                                                                                                                                                                                                                                         6
                                                                                                                                                                                                                                                                                                                                                                                                                                                                   LGVGLQDLSGDLQNS--YDNKEGAVVISVEKDSPAKKAGILVWDLITEVNGKKVKNTNEL 245
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            68 DNLPTIKFSDSNDISVGDLVFAIGNPFGVGESVTQGIVSALNKSGIGINSYENFIQTDAS 127
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                246 RNLIGSMLPNORVTLKVIRDKKERAFTLTLAERKNPNKKETISAQNGAQGQLNGLQVEDL 305
                                                                                                                                                                                                                                                                                                                         10 ALGSGVIISKD-GYIVTNNHVIDGADKIKVTIPGSNKEYSATLVGTDSESDLAVIRI-TK 67
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       306 TQETKRSMRLSDDVQGVLVSQVNENSPAEQAGFRQGNIITKIEEVEVKSVADFNHALEKY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     of Haemophilus Hin47 Protein with
                                                                                                                                                                                                                                                     DB 1; Length 472;
                                                                                                                                                                                                                                                                                         Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       GENERAL INFORMATION:
GENERAL INFORMATION:
APPLICANT: LOCSMORE, Sheena M.
APPLICANT: YANG, Yan-Ping
APPLICANT: CHONG, Pele
APPLICANT: COMEN, Raymond P.
APPLICANT: Nichel H.
TITLE OF INVENTION: Reduced Protease Activity
NUMBER OF SEQUENCES: 23
CORRESPONDENCE ADDRESS:
ADDRESSEE: Sim & MCBUINEY
STREET: Suite 701, 330 University Avenue
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           SOFTWARE: Patentin Release #1.0, Version #1.25 CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                   37.4%; Score 725.5; DB 1;
43.2%; Pred. No. 1.4e-53;
tive 75; Mismatches 114;
                                 1038-493 MIS:vg
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       COMPUTER: IBM PC compatible OPERATING SYSTEM: PC-DOS/MS-DOS
           REGISTRATION NUMBER: 24,973
REFERENCE/DOCKET NUMBER: 1038
TELECOMNUNICATION INFORMATION:
TELEPHONE: (416) 595-1155
TELEFAX: (416) 595-1163
TELEFAX: (416) 595-1163
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Sequence 5, Application US/08487167
Patent No. 5869302
Stewart, Michael I.
                                                                                                                                       LENGTH: 472 amino acids TYPE: amino acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             366 KGKPKRFLVLDLNQGYR 382
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   -SKPS-VLALNIQRGDR 467
                                                                                                                                                                                                                                                                      Best Local Similarity 43.2
Matches 163; Conservative
                                                                                                                                                                              single
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     COMPUTER READABLE FORM:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              IRY: Canada
M5G 1R7
                                                                                                                                                                                                 TOPOLOGY: linear
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          CITY: Toronto
STATE: Ontario
COUNTRY: Canada
                                                                                                                                                                              STRANDEDNESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          MEDIUM TYPE:
                                                                                                                                                                                                                US-08-472-173-5
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    US-08-487-167-5
                                                                                                                                                                                                                                                     Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            g
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              g
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ŏ
                                                                                                                                                                                                                                                                                                                                                          a
                                                                                                                                                                                                                                                                                                                                                                                              ŏ
                                                                                                                                                                                                                                                                                                                                                                                                                                  g
                                                                                                                                                                                                                                                                                                                                                                                                                                                                     à
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   g
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         à
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ò
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     δ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         В
```

```
Haemophilus Hin47 Protein with Reduced Protease A
6
```

```
; Sequence 5, Application US/08801499
                 OOMEN, Raymond P. KLEIN, Michel H.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               366 KGKPKRFLVLDLNQGYR 382
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  -SKPS-VLALNIQRGDR 467
   CHONG, Pele
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 STRANDEDNESS: single
                                                                                                                                                                                                                                                                                                                                                            CLASSIFICATION: 514
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Best Local Similarity
Matches 163; Conserva
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               TYPE: amino acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  linear
                                                                                                                                                                                      COUNTRY: Canada
ZIP: M5G 1R7
                                                                                                                                                                                                                                                                                                                                            FILING DATE:
                   APPLICANT:
APPLICANT:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  US-08-296-149-5
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                RESULT 7
US-08-801-499-5
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      89
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           246
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          351
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             453
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   g
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      δ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     g
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     g
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          δ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        g
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ò
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          g
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ò
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Q
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ŏ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       δ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  6
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  246 RNLIGSMLPNQRVTLKVIRDKKERAFTLTLAERKNPNKKETISAQNGAQGQLNGLQVEDL 305
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    128 INPGNSGALIDSRGGLVGINTAIISKTGGNHGIGFAIPSNMVKDTVTQLIKTGKIERGY 187
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     LGVGLQDLSGDLQNS--YDNKEGAVVISVEKDSPAKKAGILVWDLITEVNGKKVKNTNEL 245
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         400 ---AEMSNKGKD--OGVVVNNVKTGTPAAQIGLKKGDVIIGANQIAVKNIAEIRKVLD-- 452
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   68 DNLPTIKFSDSNDISVGDLVFAIGNPFGVGESVTQGIVSALNKSGIGINSYENFIQTDAS 127
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  10 ALGSGVIISKD-GYIVTNNHVIDGADKIKVTIPGSNKEYSATLVGTDSESDLAVIRI-TK 67
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         306 TQETKRSMRLSDDVQGVLVSQVNENSPAEQAGFRQGNIITKIEEVEVKSVADFNHALEKY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           25;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               37.4%; Score 725.5; DB 2; Length 472; 43.2%; Pred. No. 1.4e-53; tive 75; Mismatches 114; Indels 25
                                                           MEDIUM TYPE: FLOPPY disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/482,816
FILING DATE: 07-JUN-1995
CLASSIFICATION: 435
PRIOR APPLICATION NUMBER: US 08/296,149
FILING DATE: 26-AUG-1994
PRIOR APPLICATION NUMBER: US 08/296,149
FILING DATE: 21-JUL-1994
FILING DATE: 21-JUL-1994
ATPORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                NAME: Stewart, Michael I
REGISTRATION NUMBER: 24,973
REPERENCE/DCOKET NUMBER: 1038-494 MIS:vg
TELEPHONE: (416) 595-1155
TELEPHONE: (416) 595-1155
INFORMATION FOR SEQ ID NO: 5: SEQUENCE CHARACTERISTICS:
LENGTH: 472 amino acids
TYPE: amino acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         US-08-296-149-5
Sequence 5, Application US/08296149
Patent No. 5939297
GENERAL INFORMATION:
APPLICANT: LOOSMORE, Sheena M
APPLICANT: YANG, Yan-Ping
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            366 KGKPKRFLVLDLNQGYR 382
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          453 -SKPS-VLALNIORGDR 467
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Query Match
Best Local Similarity 43.2%
Matches 163; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            STRANDEDNESS: single
TOPOLOGY: linear
                                               COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy of COMPUTER: IBM PC COM
STATE: Ontario
COUNTRY: Canada
ZIP: MSG 1R7
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            US-08-482-816-5
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     188
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 g
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 q
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ó
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ó
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ð
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ద
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ò
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        8
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ŏ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         g
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            à
```

```
DNLPTIKFSDSNDISVGDLVFAIGNPFGVGESVTQGIVSALNKSGIGINSYENFIQTDAS 127
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               128 INPGNSGGALIDSRGGLVGINTAIISKTGGNHGIGFAIPSNMVKDTVTQLIKTGKIERGY 187
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   188 LGVGLQDLSGDLQNS--YDNKEGAVVISVEKDSPAKKAGILVWDLITEVNGKKVKNTNEL 245
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             RNLIGSMLPNQRVTLKVIRDKKERAFTLTLAERKNPNKKETISAQNGAQGQLNGLQVEDL 305
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             306 TQETKRSMRLSDDVQGVLVSQVNENSPAEQAGFRQGNIITKIEEVEVKSVADFNHALEKY 365
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        10 ALGSGVIISKD-GYIVTNNHVIDGADKIKVTIPGSNKEYSATLVGTDSESDLAVIRI-TK 67
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            TITLE OF INVENTION: Analog of Haemophilus Hin47 Protein with TITLE OF INVENTION: Reduced Protease Activity NUMBER OF SEQUENCES: 23 CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Length 472;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Indels
                                                                                                                                                                                                                                                                                                                                            SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/296,149
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         37.4%; Score 725.5; DB 2;
ilarity 43.2%; Pred. No. 1.4e-53;
Conservative 75; Mismatches 114;
                                                                                                       ADDRESSEE: Sim & McBurney
STREET: Sulte 701, 330 University Avenue
CITY: Toronto
STATE: Ontario
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                1038-390
                                                                                                                                                                                                                                                   COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                                                                                                                                                                                                               ATTORNEY AGENT INFORMATION:
NAME: Stewart, Michael I
REGIGSTRATTON NUMBER: 24,973
REFRENCE/DOCKET NUMBER: 1038
TELECOMMUNICATION INFORMATION:
TELEPHONE: (416) 595-1155
INFORMATION FOR SEQ ID NO: 5:
SEQUENCE CHARACTERISTICS:
LENGTH: 472 amino acids
```

<u>ن</u>

S

```
306 TQETKRSMRLSIDVQGVLVSQVNENSPAEQAGFRQGNIITKIEEVEVKSVADFNHALEKY 365
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         LGVGLQDLSGDLKINS--YDNKEGAVVISVEKDSPAKKAGILVWDLITEVNGKKVKNTNEL 245
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      DNLPTIKFSDSNI) ISVGDLVFAIGNPFGVGESVTQGIVSALNKSGIGINSYENFIQTDAS 127
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                128 INPGNSGALIDURGGLVGINTAIISKTGGNHGIGFAIPSNMVKDTVTQLIKTGKIERGY 187
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    10 ALGSGVIISKD-(3YIVTNNHVIDGADKIKVTIPGSNKEYSATLVGTDSESDLAVIRI-TK 67
                           25;
                                                                                                                                                                                                             Sequence 5, Application US/08615271
Patent No. 5981503
GENERAL INFORMATION:
APPLICANT: LOOSMORE, Sheena M.
APPLICANT: CHONG, Pele
APPLICANT: CHONG, Pele
APPLICANT: KLEIM, Michel H.
TITLE OF INVENTION: ANALOG OF HAEMOPHILUS HIN47 WITH REDUCED
TITLE OF INVENTION: PROTEASE ACTIVITY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Length 472;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              SOFTWARE: Patentin Release #1.0, Version #1.30 CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/615,271 FILING DATE: 20-JUN-1996 CLASSIFICATION: 514
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Query Match 37.4%; Score 725.5; DB 2; Best Local Similarity 43.2%; Pred. No. 1.4e-53; Matches 163; Conservative 75; Mismatches 114;
                                                                                                                                                                                                                                                                                                                                                                                                                                                               ADDRESSEE: Sim & McBurney
STREET: 6th Floor, 330 University Avenue
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ATTORNEY/AGENT INFORMATION:
NAME: Stewart, Michael I
REGISTRATION NUMBER: 24,973
REFERENCE/DGCKET NUMBER: 1038-580
TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-OOS/MS-DOS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  TELEPHONE: (415) 595-1155
TELEFAX: (416) 595-1163
INFORMATION FOR SEQ ID NO: 5:
                                                                               366 KGKPKRFLVLDI,NQGYR 382
                                                                                                        LENGTH: 472 amino acids
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      STRANDEDNESS: single
TOPOLOGY: linear
                                                                                                                                                                                                                                                                                                                                                                                                                       NUMBER OF SEQUENCES: CORRESPONDENCE ADDRESS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    CITY: Toronto
STATE: Ontario
COUNTRY: Canada
ZIP: M5G 1R7
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Query Match
                                                                                                                                                                                                   US-08-615-271-5
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                US-08-615-271-5
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 89
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  188
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       291
                                       a
                                                                               à
                                                                                                                g
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ŏ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          g
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ŏ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         q
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ŏ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    g
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ò
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     g
    à
                                                      APPLICANT: YANG, Yan-Ping
APPLICANT: CHONG, Pele
APPLICANT: OCHEN, Pele
APPLICANT: NICHOL P.
APPLICANT: KLEIN, Michel H.
TITLE OF INVENTION: Analog of Haemophilus Hin47 Protein with Reduced Protease Act
CORRESPONDENCES: 23
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  .
б
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     DNLPTIKFSDSNDISVGDLVFAIGNPFGVGESVTQGIVSALNKSGIGINSYENFIQTDAS 127
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 INPGNSGGALIDSRGGLVGINTAIISKTGGNHGIGFAIPSNMVKDTVTQLIKTGKIERGY 187
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        LGVGLQDLSGDLQNS--YDNKEGAVVISVEKDSPAKKAGILVWDLITEVNGKKVKNTNEL 245
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               RNLIGSMLPNQRVTLKVIRDKKERAFTLTLAERKNPNKKETISAQNGAQGQLNGLQVEDL 305
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   10 ALGSGVIISKD-GYIVTNNHVIDGADKIKVTIPGSNKEYSATLVGTDSESDLAVIRI-TK 67
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    37.4%; Score 725.5; DB 2; Length 472; 43.2%; Pred. No. 1.4e-53; Live 75; Mismatches 114; Indels 25.
                                                                                                                                                                                                                                                                                                                                                                                              SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/801,499
                                                                                                                                                                                             ADDRESSEE: Sim & McBurney
STREET: 6th Floor, 330 University Avenue
CITY: Toronto
STATE: Ontario
COUNTRY: Canada
COUNTRY: Canada
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             1038-671 MIS:jb
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/482,816
FILING DATE: 07-JUN-1995
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/296,149
FILING DATE: 26-AUG-1994
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/278,091
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       APPLICATION NUMBER: US 08/278,091
FILING DATE: 21-JUL-1994
ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                         COMPUTER: IBM PC compatible OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      NAME: Stewart, Michael I
REGISTRATION NUMBER: 24,973
REFERENCE/DOCKET NUMBER: 105
TELECOMMUNICATION INFORMATION:
TELEPHONE: (416) 595-1155
TELEFAX: (416) 595-1163
                  GENERAL INFORMATION:
APPLICANT: LOOSMORE, Sheena M
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            TELEPHONE: (416) 595-1155
TELEFAX: (416) 595-1163
INFORMATION FOR SEQ ID NO: 5:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                LENGTH: 472 amino acids
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Best Local Similarity 43.2
Matches 163; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                TYPE: amino acid
STRANDEDNESS: single
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  CLASSIFICATION: 514
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ; TOPOLOGY: linear
US-08-801-499-5
Patent No. 5962430
                                                                                                                                                                                                                                                                                                                                                                                                                                                               FILING DATE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  89
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 128
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                188
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    291
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             246
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     351
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        d
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     q
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ŏ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ŏ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ŏ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    a
```

ó

```
US-09-074-659-5
                                                                                                                                                                                                                                   246
                                                                                                                                                                                               g
                                                                                                                                                                                                                                                                    q
                                                                                         õ
                                                                                                                       g
                                                                                                                                                                õ
                                                                                                                                                                                                                                                                                                           ò
                                                                                                                                                                                                                                                                                                                                             a
                                                                                                                                                                                                                                                                                                                                                                                δ
                                                                                                                                                                                                                                                                                                                                                                                                                g
                                                                                                                                                                                                                                       à
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 6
246 RNLIGSMLPNORVTLKVIRDKKERAFTLTLAERKNPNKKETISAONGAOGOLNGLOVEDL 305
                                                                    306 TQETKRSMRLSDDVQGVLVSQVNENSPAEQAGFRQGNIITKIEEVEVKSVADFNHALEKY 365
                                                                                         Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                10 ALGSGVIISKD-GYIVTNNHVIDGADKIKVTIPGSNKEYSATLVGTDSESDLAVIRI-TK 67
                  25;
                                                                                                                                                                                                                                                                                                                                                                                                                TITLE OF INVENTION: Analog of Haemophilus Hin47 Protein with TITLE OF INVENTION: Reduced Protease Activity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               75; Mismatches 114; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          COMPUTER REALABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
APPLICATION NUMBER: US/09/074,660
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                1.4e-53;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       E: Sim & McBurney
6th Floor, 330 University Avenue
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           1038-731 MIS:jb
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Query Match 37.4%; Score 725.5; Best Local Similarity 43.2%; Pred. No. 1.46 Matches 163; Conservative 75; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/487,167
FILING DATE: 07-JUN-1995
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/296,149
FILING DATE: 26-AUG-1994
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/278,091
FILING DATE: 21-JUL-1994
ATTORNEY AGENT INFORMATION:
                                                                                                                                                                                                                                                                    ; Sequence 5, Application US/09074660
; Patent No. 6020183
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   NAME: Stewart, Michel I.
REGISTRATION NUMBER: 24,973
REFERENCE/DOCKET NUMBER: 1038
TELECOMMUNICATION INFORMATION:
TELEPHONE: (416) 595-1153
INFORMATION FOR SEQ ID NO: 5:
SEQUENCE CHARACTERISTICS:
LENGTH: 472 amino acids
                                                                                                                                                                                                                                                                                                    GENERAL INFORMATION:
APPLICANT: LOOSMORE, Sheena M.
APPLICANT: YANG, Yan-Ping
APPLICANT: CHONG, Pele
APPLICANT: CHONG, RAYMONG P.
APPLICANT: KLEIN, Michel H.
                                                                                                                                                                                                                                                                                                                            LOOSMORE, Sheena M.
                                                                                                                                           366 KGKPKRFLVLDLNQGYR 382
                                                                                                                                                                             453 -SKPS-VLALNIQRGDR 467
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
                                                                                                                                                                                                                                                                                                                                                                                                                                                    NUMBER OF SEQUENCES: CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           E: Ontario
FRY: Canada
M5G 1R7
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              STREET: btn ...
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         CLASSIFICATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       FILING DATE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ADDRESSEE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            COUNTRY:
                                                                                                                                                                                                                                                    US-09-074-660-5
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        US-09-074-660-5
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            CITY: STATE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                q
                                                                                                      g
ò
                                 임
                                                                    ŏ
                                                                                                                                           ò
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ò
```

```
68 DNLPTIKFSDSNDISVGDLVFAIGNPFGVGESVTQGIVSALNKSGIGINSYENFIQTDAS 127
                                                                                              128 INPGNSGGALIDSRGGLVGINTAIISKTGGNHGIGFAIPSNMVKDTVTQLIKTGKIERGY 187
                                                                                                                                                                                                                                                                                             RNLIGSMLPNORVTLKVIRDKKERAFTLTLAERKNPNKKETISAQNGAQGQLNGLQVEDL 305
                                                                                                                                                                                                 188 LGVGLQDLSGDLQNS--YDNKEGAVVISVEKDSPAKKAGILVWDLITEVNGKKVKNTNEL
                                                                                                                                                                                                                                                                                                                 306 TQETKRSMRLSDDVQGVLVSQVNENSPAEQAGFRQGNIITKIEEVEVKSVADFNHALEKY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              TITLE OF INVENTION: Analog of Haemophilus Hin47 Protein with TITLE OF INVENTION: Reduced Protease Activity NUMBER OF SEQUENCES: 23 CORRESPONDENCE ADDRESS: ADDRESS: Sim & MCBurney
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    SOFTWARE: Patentin Release #1.0, Version #1.25 CURRENT APPLICATION DATA: APPLICATION NUMBER: US/09/074,659
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ADDRESSEE: Sim & McBurney
STREET: 6th Floor, 330 University Avenue
CITY: Torontco
STATE: Ontario
COUNTRY: Canada
ZIP: MGS IR?
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
COMPUTER: IBM PC compatible
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   NAME: Stewart, Michael I.
REGISTRATION NUMBER: 24,973
REFERENCE/DOCKET NUMBER: 1038-730 MIS: jb
TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     CLASSIFICATION:
CLASSIFICATION:
PRIOR APPLICATION NUMBER: US 08/487,167
FILING DATE: 07-UNN-1995
PRIOR APPLICATION NUMBER: US 08/296,149
FILING DATE: 26-NG-1994
FILING DATE: 26-NG-1994
FILING DATE: 21-UL-1994
FILING DATE: 21-UL-1994
ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Sequence 5, Application US/09074659 Patent No. 6025342
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               GENERAL INFORMATION:
APPLICANT: LOOSMORE, Sheena M.
APPLICANT: YANG, Yan-Ping
APPLICANT: CHONG, PEL
APPLICANT: OOMEN, Raymond P.
APPLICANT: KLEIN, Michel H.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              TELEPHONE: (416) 595-1155
TELEFAX: (416) 595-1163
INFORMATION FOR SEQ ID NO: 5:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              366 KGKPKRFLVLDLNQGYR 382
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            453 -SKPS-VLALNIQRGDR 467
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     FILING DATE:
```

```
Stewart, Michael I
                                                                                                                                             STRANDEDNESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ADDRESSEE:
                                                                                                                                                                TOPOLOGY:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             US-09-106-466A-5
                                                                                                                                                                            US-09-106-468-5
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          STREET:
                                                                                                                                                                                                           Query Match
                                                                                                                                                                                                                                                                                                                          68
                                                                                                                                                                                                                                                                                                                                                                                    128
                                                                                                                                                                                                                                                                                                                                                                                                                                              188
                                                                                                                                                                                                                                                                                                                                                                                                                                                                          291
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 306
                                                                                                                                                                                                                                                                     õ
                                                                                                                                                                                                                                                                                             g
                                                                                                                                                                                                                                                                                                                          ò
                                                                                                                                                                                                                                                                                                                                                     g
                                                                                                                                                                                                                                                                                                                                                                                    ò
                                                                                                                                                                                                                                                                                                                                                                                                               g
                                                                                                                                                                                                                                                                                                                                                                                                                                            ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                        g
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       õ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                g
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Ω
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          g
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         οy
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   a
                                                                                                                    6
                                                                                                                                                                245
                                                                                                                                                                                                                                                                                                                                        306 TQETKRSMRLSDDVQGVLVSQVNENSPAEQAGFRQGNIITKIEEVEVKSVADFNHALEKY 365
                                                                                                                                                                                                                                                                                                                                                                                                                                                             68 DNLPTIKFSDSNDISVGDLVFALGNPFGVGESVTQGIVSALNKSGIGINSYENFIQTDAS 127
                                                                                                                                                                                                                                                                128 INPGNSGALIDSRGGLVGINTAIISKTGGNHGIGFAIPSNMVKDTVTQLIKTGKIERGY 187
                                                                                                                                                                                                                                                                                                                                                                                  RNLIGSMLPNQRVTLKVIRDKKERAFTLTLAERKNPNKKETISAQNGAQGQLNGLQVEDL 305
                                                                                                                     Gaps
                                                                                                                                             10 ALGSGVIISKD-GYIVTNNHVIDGADKIKVTIPGSNKEYSATLVGTDSESDLAVIRI-TK 67
                                                                                                                                                                                                                                                                                                                        LGVGLQDLSGDLQNS--YDNKEGAVVISVEKDSPAKKAGILVWDLITEVNGKKVKNTNEL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                APPLICANT: LOOSWORE, Sheena M.
APPLICANT: YANG, Yan-Ping
APPLICANT: CHONG, Pele
APPLICANT: CHONG, Pele
APPLICANT: Michel H.
APPLICANT: KLEIN, Michel H.
APPLICANT: NIEN, MICHEL H.
APPLICANT: TILLE OF INVENTION: PROFDESE ACTIVITY
                                                                                        Length 472;
                                                                                                                    Indels
                                                                                   37.4%; Score 725.5; DB 3;
43.2%; Pred. No. 1.4e-53;
tive 75; Mismatches 114;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                SOFTWARE: PatentIn Release #1.0, Version #1.30 CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ADDRESSEE: Sim & McBurney
STREET: 6th Floor, 330 University Avenue
CITY: Toronto
STATE: Ontario
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           APPLICATION NUMBER: US 08/615,271 FILING DATE: 20-JUN-1996 CLASSIFICATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   APPLICATION NUMBER: US/09/106,468
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Sequence 5, Application US/09106468 Patent No. 6114125 GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ATTORNEY/AGENT INFORMATION:
LENGTH: 472 amino acids
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    366 KGKPKRFLVLDLNQGYR 382
                                                                                                                  Matches 163; Conservative
               ; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
US-09-074-659-5
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              PRIOR APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        NUMBER OF SEQUENCES: CORRESPONDENCE ADDRESS:
                                                                                     Query Match
Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             COUNTRY: Canada
ZIP: M5G 1R7
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  FILING DATE:
CLASSIFICATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          US-09-106-468-5
                                                                                                                                                                                                                                   171
                                                                                                                                                                                                                                                                                                                        188
                                                                                                                                                                                                                                                                                                                                                                                  246
                                                                                                                                                                                                                                                                ò
                                                                                                                                                                                                                                                                                          g
                                                                                                                                                                                                                                                                                                                                                    g
                                                                                                                                                                                                                                                                                                                                                                                                            g
                                                                                                                                                                                                                                                                                                                                                                                                                                                                        q
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               g
                                                                                                                                                                          g
                                                                                                                                                                                                       ð
                                                                                                                                                                                                                                                                                                                        ò
                                                                                                                                                                                                                                                                                                                                                                                  õ
                                                                                                                                                                                                                                                                                                                                                                                                                                            ò
                                                                                                                                               ò
```

```
171 KNLTAIKMADSDALRVGDYTVGIGNPFGLGETVTSGIVSALGRSGLNAENYENFIQTDAA 230
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           LGVGLQDLSGDLJNS--YDNKEGAVVISVEKDSPAKKAGILVWDLITEVNGKKVKNTNEL 245
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           DNLPTIKFSDSNDISVGDLVFAIGNPFGVGESVTQGIVSALNKSGIGINSYENFIQTDAS 127
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     INPGNSGGALIDSRGGLVGINTAIISKTGGNHGIGFAIPSNMVKDTVTQLIKTGKIERGY 187
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           RNLIGSMLPNQRVTLKVIRDKKERAFTLTLAERKNPNKKETISAQNGAQGQLNGLQVEDL 305
                                                                                                                                                                                                                                                                                                                                                                                               10 ALGSGVIISKD-GYIVTNNHVIDGADKIKVTIPGSNKEYSATLVGTDSESDLAVIRI-TK 67
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      TOETKRSMRLSDDVQGVLVSQVNENSPAEQAGFRQGNIITKIEEVEVKSVADFNHALEKY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    OF HAEMOPHILUS HIN47 WITH REDUCED
                                                                                                                                                                                                                                                                                                     37.4%; Score 725.5; DB 3; Length 472; 43.2%; Pred. No. 1.4e-53;
                                                                                                                                                                                                                                                                                                                                                   Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PATENTIN Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                 75; Mismatches 114;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   :: Sim & McBurney
6th Floor, 330 University Avenue
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  TITLE OF INVENTION: ANALOG OF HAEMOPH TITLE OF INVENTION: PROTEASE ACTIVITY
                        1038-825
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Sequence 5, Application US/09106466A Patent No. 6147057
                REFERENCE/DOCKET NUMBER: 1036
TELECOMMUNICATION INFORMATION:
TELEPHONE: (416) 595-1155
TELEFAX: (416) 595-1163
INFORMATION FOR SEQ ID NO: 5:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     GENERAL INFORMATION:
APPLICANT: LOOSMORE, Sheena M.
APPLICANT: TANG, Yan-Ping
APPLICANT: CHONG, Pele
APPLICANT: COMEN. Raymond P.
APPLICANT: KLEIN, Michel H.
24,973
                                                                                                                                                             LENGTH: 472 amino acids TYPE: amino acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 366 KGKPKRFLVLDLNQGYR 382
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            453 -SKPS-VLALNIARGDR 467
                                                                                                                                                                                                                                                                                                                                                   Matches 163; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  STATE: Ontario
COUNTRY: Canadu
ZIP: MSG 1R7
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy d
  REGISTRATION NUMBER:
                                                                                                                                                                                                              single
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   NUMBER OF SEQUENCES: CORRESPONDENCE ADDRESS
                                                                                                                                                                                                                                    linear
                                                                                                                                                                                                                                                                                                                             Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Toronto
```

```
DNLPTIKFSDSNDISVGDLVFAIGNPFGVGESVTQGIVSALNKSGIGINSYENFIQTDAS 127
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   128 INPGNSGGALIDSRGGLVGINTAIISKTGGNHGIGFAIPSNMVKDTVTQLIKTGKIERGY 187
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           188 LGVGLQDLSGDLQNS--YDNKEGAVVISVEKDSPAKKAGILVWDLITEVNGKKVKNTNEL 245
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      RNLIGSMLPNORVTLKVIRDKKERAFTLTLAERKNPNKKETISAQNGAQGQLNGLQVEDL 305
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 306 TQETKRSMRLSDDVQGVLVSQVNENSPAEQAGFRQGNIITKIEEVEVKSVADFNHALEKY 365
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 10 ALGSGVIISKD-GYIVTNNHVIDGADKIKVTIPGSNKEYSATLVGTDSESDLAVIRI-TK 67
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Length 472;
                                                COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/106,467
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Query Match 37.4%; Score 725.5; DB 4; Best Local Similarity 43.2%; Pred. No. 1.4e-53; Matches 163; Conservative 75; Mismatches 114;
                                                                                                                                                                                                                                                                                                          CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/615,271
FILING DATE: 20-JUN-1996
CLASSIFICATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   1038-824
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               NAME: Stewart, Michael I
REGISTRATION NUMBER: 24,973
REFRENCE/DOCKET NUMBER: 1038
TELECOMMUNICATION INFORMATION:
TELEPHONE: (416) 595-1155
TELEPHONE: (416) 595-1163
INFORMATION FOR SEQ ID NO: 5:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Sequence 6, Application US/08278091
Patent No. 5506139
GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   LOOSMORE, Sheena M
YANG, Yan-Ping
CHONG, Pele
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              KLEIN, Michel H.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         366 KGKPKRFLVLDLNQGYR 382
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                -SKPS-VLALNIQRGDR 467
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               TYPE: amino acid
STRANDEDNESS: single
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       TOPOLOGY: linear
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              COMEN,
                                                                                                                                                                                                                                                                                      FILING DATE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   APPLICANT: I
APPLICANT: Y
APPLICANT: C
APPLICANT: C
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              US-08-278-091-6
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      246
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           89
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   351
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      453
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     q
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ò
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             셤
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              à
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        셤
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ò
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                g
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ò
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ò
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            6
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   128 INPGNSGGALIDSRGGLVGINTAIISKTGGNHGIGFAIPSNMVKDTVTQLIKTGKIERGY 187
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               246 RNLIGSMLPNQRVTLKVIRDKKERAFTLTLAERKNPNKKETISAQNGAQGQLNGLQVEDL 305
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       306 TQETKRSMRLSDDVQGVLVSQVNENSPAEQAGFRQGNIITKIEEVEVKSVADFNHALEKY 365
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              68 DNLPTIKFSDSNDISVGDLVFAIGNPFGVGESVTQGIVSALNKSGIGINSYENFIQTDAS 127
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                10 ALGSGVIISKD-GYIVTNNHVIDGADKIKVTIPGSNKEYSATLVGTDSESDLAVIRI-TK 67
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        188 LGVGLQDLSGDLQNS--YDNKEGAVVISVEKDSPAKKAGILVWDLITEVNGKKVKNTNEL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   | :|| :|| :|| :-|| |- || |- || |- || |- || |- || |- || |- || |- || |- || |- || |- || |- || |- || |- || |- || |- || |- || |- || |- || |- || |- || |- || |- || |- || |- || |- || |- || |- || |- || |- || |- || |- || |- || |- || |- || |- || |- || |- || |- || |- || |- || |- || |- || |- || |- || |- || |- || |- || |- || |- || |- || |- || |- || |- || |- || |- || |- || |- || |- || |- || |- || |- || |- || |- || |- || |- || |- || |- || |- || |- || |- || |- || |- || |- || |- || |- || |- || |- || |- || |- || |- || |- || |- || |- || |- || |- || |- || |- || |- || |- || |- || |- || |- || |- || |- || |- || |- || |- || |- || |- || |- || |- || |- || |- || |- || |- || |- || |- || |- || |- || |- || |- || |- || |- || |- || |- || |- || |- || |- || |- || |- || |- || |- || |- || |- || |- || |- || |- || |- || |- || |- || |- || |- || |- || |- || |- || |- || |- || |- || |- || |- || |- || |- || |- || |- || |- || |- || |- || |- || |- || |- || |- || |- || |- || |- || |- || |- || |- || |- || |- || |- || |- || |- || |- || |- || |- || |- || |- || |- || |- || |- || |- || |- || |- || |- || |- || |- || |- || |- || |- || |- || |- || |- || |- || |- || |- || |- || |- || |- || |- || |- || |- || |- || |- || |- || |- || |- || |- || |- || |- || |- || |- || |- || |- || |- || |- || |- || |- || |- || |- || |- || |- || |- || |- || |- || |- || |- || |- || |- || |- || |- || |- || |- || |- || |- || |- || |- || |- || |- || |- || |- || |- || |- || |- || |- || |- || |- || |- || |- || |- || |- || |- || |- || |- || |- || |- || |- || |- || |- || |- || |- || |- || |- || |- || |- || |- || |- || |- || |- || |- || |- || |- || |- || |- || |- || |- || |- || |- || |- || |- || |- || |- || |- || |- || |- || |- || |- || |- || |- || |- || |- || |- || |- || |- || |- || |- || |- || |- || |- || |- || |- || |- || |- || |- || |- || |- || |- || |- || |- || |- || |- || |- || |- || |- || |- || |- || |- || |- || |- || |- || |- || |- || |- || |- || |- || |- || |- || |- || |- || |- || |- || |- || |- || |- || |- || |- || |- || |- || |- || |- || |- || |- || |- || |- || |- || |- || |- || |- ||
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Sequence 5, Application US/09106467
Patent No. 6153580
GENERAL INFORMATION:
APPLICANT: LOOSMORE, Sheena M.
APPLICANT: YANG, Yan-Ping
APPLICANT: CHONG, Pele
APPLICANT: OMEN, Raymond P.
APPLICANT: KLEIN, Michel H.
TITLE OF INVENTION: ANALOG OF HAEMOPHILUS HIN47 WITH REDUCED
TITLE OF INVENTION: PROTEASE ACTIVITY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              DB 4; Length 472;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        37.4%; Score 725.5; DB 4; Length 43.2%; Pred. No. 1.4e-53; Live 75; Mismatches 114; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             CORRESPONDENCE ADDRESS:
ADDRESSEE: Sim & McBurney
STREET: 6th Floor, 330 University Avenue
APPLICATION NUMBER: US/09/106,466A
                             FILING DATE:
CLASSIFICATION: 514514
PCLASSIFICATION DATA:
APPLICATION NUMBER: US 08/615,271
FILING DATE: 20-JUN-1996
FILING DATE: 314514
                                                                                                                                                                                                        ATTORNEY/AGENT INFORMATION:
NAME: Stewart, Michael I
REGISTATION UNDRER: 24,913
REFERENCE/DOCKET UNBER: 1038
TELECOMMUNICATION INFORMATION:
TELEFAX: (416, 595-1155
TELEFAX: (416, 595-1155
SEQUENCE CHARACTERISTICS:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            LENGTH: 472 amino acids
TYPE: amino acid
STRANDEDNESS: single
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   366 KGKPKRFLVLDLNQGYR 382
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             453 -SKPS-VLALNIQRGDR 467
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Best Local Similarity 43.28
Matches 163; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      NUMBER OF SEQUENCES:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ; TOPOLOGY: linear
US-09-106-466A-5
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Abbara
STREET: bear
Toronto
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        US-09-106-467-5
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           CITY: STATE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          g
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     a
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       g
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        à
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ò
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       g
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  q
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        à
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ŏ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ò
```

ö

```
366 KGKPKRFLVLDLNQG 380
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Query Match
Best Local 3
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          g
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  g
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Qγ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              q
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Ω
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ŏ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        a
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ò
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    g
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      δλ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 g
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ò
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  6
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          LGVGLQDLSGDLQNS--YDNKEGAVVISVEKDSPAKKAGILVWDLITEVNGKKVKNTNEL 245
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           RNLIGSMLPNQRVTLKVIRDKKERAFTLTLAERKNPNKKETISAQNGAQGQLNGLQVEDL 305
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 | :|:| ::| ::| ::|: | | | |: |
352  RAQYGTMPVGSKISLGLLREGK--AITVNL-------ELQQSSQSQVDSSTIFSG 397
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               DNLPTIKFSDSNDISVGDLVFAIGNPFGVGESVTQGIVSALNKSGIGINSYENFIQTDAS 127
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       128 INPGNSGALIDSRGGLVGINTALISKTGGNHGIGFAIPSNMVKDTVTQLIKTGKIERGY 187
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              10 ALGSGVIISKD-GYIVTNNHVIDGADKIKVTIPGSNKEYSATLVGTDSESDLAVIRI-TK 67
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Analog of Haemophilus Hin47 Protein with
Reduced Protease Activity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Length 475;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                37.4%; Score 724.5; DB 1; Length 4 43.2%; Pred. No. 1.7e-53; Live 74; Mismatches 114; Indels
                                                                                                                                                               MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPFRAING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
FILING DATE: 21-JUL-1994
CLASSIFICATION: 435
                                                           ADDRESSEE: Sim & McBurney
STREET: Suite 701, 330 University Avenue
CITY: Toronto
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Sequence 6, Application US/08483859
Patent No. 5656436
GENERAL INFORMATION:
APPLICANT: LOOSMORE, Sheena M.
                                                                                                                                                                                                                                                                                           ATTORNEY/AGENT INFORMATION:
NAME: Stewart, Michael I
REGISTRATION NUMBER: 24,973
REFERENCE/DOCKET NUMBER: 10
TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                         TELEPHONE: (416) 595-1155
TELEFAX: (416) 595-1163
INFORMATION FOR SEQ ID NO: 6:
SEQUENCE GHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                        LENGTH: 475 amino acids
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Query Match 37.4%
Best Local Similarity 43.2%
Matches 162; Conservative
                                                                                       CITY: Toronto
STATE: Ontario
COUNTY: Canada
ZIP: M5G 1R7
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy di
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          366 KGKPKRFLVLDLNQG 380
                                                                                                                                                                                                                                                                                                                                                                                                                                                                        single
TITLE OF INVENTION: An TITLE OF INVENTION: RE NUMBER OF SEQUENCES: 2 CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                        amino acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     linear
                                                                                                                                                                                                                                                                                                                                                                                                                                                                      STRANDEDNESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    US-08-483-859-6
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         68
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    232
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  188
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               292
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                246
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            셤
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ŏ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ò
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  d
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ŏ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               g
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              δ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        g
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          δŽ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       g
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ò
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               å
```

```
68 DNLPTIKFSDSNIISVGDLVFAIGNPFGVGESVTQGIVSALNKSGIGINSYENFIQTDAS 127
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            128 INPGNSGGALIDSRGGLVGINTAIISKTGGNHGIGFAIPSNMVKDTVTQLIKTGKIERGY 187
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             188 LGVGLQDLSGDL@NS--YDNKEGAVVISVEKDSPAKKAGILVWDLITEVNGKKVKNTNEL 245
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          246 RNLIGSMLPNQRVTLKVIRDKKERAFTLTLAERKNPNKKETISAQNGAQGQLNGLQVEDL 305
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                10 ALGSGVIISKD-GYIVTNNHVIDGADKIKVTIPGSNKEYSATLVGTDSESDLAVIRI-TK 67
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           306 TQETKRSMRLSDI/VQGVLVSQVNENSPAEQAGFRQGNIITKIEEVEVKSVADFNHALEKY
                                                                                        TITLE OF INVENTION: Analog of Haemophilus Hin47 Protein with TITLE OF INVENTION: Reduced Protease Activity NUMBER OF SEQUENCES: 23
CORRESPONDENCE ADIRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Length 475;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Indels
                                                                                                                                                                                                                                                                                                                                                                                                                        Patentin Release #1.0, Version #1.25
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            h 37.4%; Score 724.5; DB 1; Similarity 43.2%; Pred. No. 1.7e-53; 62; Conservative 74; Mismatches 114;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           NAME: Stewart, Michael I.
REGISTRATION NUMBER: 24,973
REFERENCE/DOCKET NUMBER: 1038-495 MIS:v9
                                                                                                                                                                                       E: Sim & McBurney
Suite 701, 330 University Avenue
                                                                                                                                                                                                                                                                                                                                                                                                                                       CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/483,859
FILING DATE: 07-UN-1995
CLASSIFFICATION NUMBER: US 08/296,149
APPLICATION NUMBER: US 08/296,149
FILING DATE: 26-AUG-1994
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/296,149
FILING DATE: 26-AUG-1994
ATTORNEY, AGENT: INFORMATION:
ATTORNEY, AGENT INFORMATION:
                                                                                                                                                                                                                                                                             COUNTRY: Canada
ZIP: M5G 1R7
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM FC Compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               TELECOMMUNICATION INFORMATION
                                            APPLICANT: OOMEN, Raymond P. APPLICANT: KLEIN, Michel H.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        TELEPHONE: (416, 595-1155
TELEFAX: (416) 595-1163
INFORMATION FOR SEQ ID NO: 6:
YANG, Yan-Ping
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       475 ami.no acids
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               SEQUENCE CHARACTERISTICS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ; ' TOPOLOGY: linear
US-08-483-859-6
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             amino acid
                                                                                                                                                                                                                              CITY: Toronto
STATE: Ontario
COUNTRY: Canada
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             TYPE: amino a STRANDEDNESS:
                                                                                                                                                                                  ADDRESSEE:
                                                                                                                                                                                                                                                                                                                                                                                                                             SOFTWARE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Matches 162;
```

Search completed: November 18, 2002, 11:30:31 Job time : 19 secs

```
November 18, 2002, 11:33:46; Search time 18 Seconds (without alignments) 632.593 Million cell updates/sec
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.
                                                                                                                                                                                                                                                                 US-09-895-913A-120
387
1 MIPKERMERALGSGVIISKD.......RPKRFLVLDLNQGYRIILVK 387
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           /cgn2_6/ptodata/1/laa/5A_COMB.pep:*
/cgn2_6/ptodata/1/laa/5B_COMB.pep:*
/cgn2_6/ptodata/1/laa/6A_COMB.pep:*
/cgn2_6/ptodata/1/laa/6B_COMB.pep:*
/cgn2_6/ptodata/1/laa/PCTUS_COMB.pep:*
/cgn2_6/ptodata/1/laa/PCTUS_COMB.pep:*
GenCore version 5.1.3
Copyright (c) 1993 - 2002 Compugen Ltd.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Total number of hits satisfying chosen parameters:
                                                                                                                                                                                                                                                                                                                                                                                                                                                              262574 seqs, 29422922 residues
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Post-processing: Listing first 45 summaries
                                                                                                        OM protein - protein search, using sw model
                                                                                                                                                                                                                                                                                                                                                                                  OLIGO
Gapop 60.0 , Gapext 60.0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Issued_Patents_AA:*
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Minimum DB seq length: 0
Maximum DB seq length: 200000000
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    0
                                                                                                                                                                                                                                                                                                Perfect score:
Sequence:
                                                                                                                                                                                                                                                                                                                                                                                  coring table:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Word size :
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Database:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Searched:
                                                                                                                                                              Run on:
                                                                                                                                                                                                                                                                         Title:
```

GENERAL INFORMATION:

APPLICANT: KTIVAN, Howard C.
APPLICANT: KTIVAN, James E.
TITLE OF INVENTION: ADHESIN-OLIGOSACCHARIDE CONJUGATE
TITLE OF INVENTION: VACCINE FOR HAEMOPHILUS INFLUENZAE
NUMBER OF SEQUENCES: 2
CORRESPONDENCE ADDRESS:

Sequence 2, Application US/08485569 Patent No. 5679547

RESULT 1 US-08-485-569-2 E: Pennie & Edmonds 1155 Avenue of Americas

ADDRESSEE: STREET: 11

New York New York XY: U.S.A.

COUNTRY:

CITY: N STATE:

```
Appli
Appli
Appli
Appli
Appli
Appli
Appli
                                            Appli
Appli
Appli
Appli
Appli
                                  Appli
Appli
                                                                                                   Appli
                                                                                                             Appli
                         Sequence 2, Appli
                                                                                                         Appli
                                                                                                                   Appli
                             Sequence 2,
Sequence 2,
Sequence 5,
Sequence 5,
              Description
                                                      Sequence
Sequence
                                                                Sequence
Sequence
Sequence
                                                                                    Sequence
Sequence
Sequence
Sequence
                                                                                                                                  Sequence (
                                                                                                                                                      Sequence (
                                                                                                        Sequence
                                                  Sequence
                                                                                                                             Sequence
                                                                                                                                                 Sequence
                                                                               Sequence
                                                                                                                  Sequence
                                                                                                                        Sequence
                                                                                                                                             Sequence
                                                                US-08-296-149-5
US-08-801-499-5
US-08-615-271-5
US-09-074-660-5
                                                           -08-482-816-5
                                                                                   -09-074-659-5
                                                                                                        -08-278-091-6
-08-483-859-6
                                                                                                                  -08-472-173-6
                                                                                                                                                      US-08-615-271-6
US-09-074-660-6
                                                                                                                                                     -08-615-27
SUMMARIES
              DB
         Query
Match Length
                             Result
                                                 Š.
```

COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk

MEDIUM TYPE: Floppy disk

COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk

COMPUTER IBM PC Compatible

COMPUTER IBM PC Compatible

COMPUTER STATEM: PC-DOS/MS-DOS

SOFTWARE: PatentIn Release #1.0, Version #1.25

SUSTWARE: PAPLICATION DATA:

APPLICATION NUMBER: US/08/485,569

FILING DATE: 07-JUN-1995

RIING DATE: 27-JUN-1995

PRIOR APPLICATION DATA:

APPLICATION NUMBER: US 07/903,079

FILING DATE: 27-JUN-1992

PRIOR APPLICATION DATA:

APPLICATION NUMBER: US 07/810,966

FILING DATE: 21-DEC-1991

PRIOR APPLICATION DATA:

APPLICATION NUMBER: US 07/631,698

FILING DATE: 21-DEC-1990

ATTORNEY/AGENT INFORMATION:

NAME: BAIGAMIN, GET-ALION:

REGISTRATION WUMBER: 7969-049

TELECOMMUNICATION INFORMATION:

PET ENDANDIN INFORMATION:

PET ENDANDIN CATION INFORMATION INFORM

TELEPHONE: (21.2) 790-9090 TELEFAX: (21.2) 869-8864/9741 TELEX: 66141 PENNIE INFORMATION FOR SEQ ID NO: 2:

SEQUENCE CHARACTERISTICS: LENGTH: 463 amino acids TYPE: amino acid

STRANDEDNESS: unknown TOPOLOGY: unknown MOLECULE TYPE: protein

o, Appli 6, Appli 14, Appli 14, Appli 3, Appli 3, Appli 8, Appli 8, Appli 8, Appli 8, Appli 135, Appli 75, Appli 75, Appli 76, Appli
sednence sed
US-09-106-468-6 US-09-106-468-6 US-09-106-468-6 US-09-106-468-6 US-08-923-4648-14 US-08-923-4548-14 US-08-923-94-8 US-08-474-499-8 US-08-377-2794-8 US-08-377-2794-8 US-09-525-310-8 PCT-US95-06211-8 US-09-525-311-76 US-09-818-112-75 US-09-056-556-75
このよみのこのここことによみよみな
0.000000000000000000000000000000000000
200000000000000000000000000000000000000
0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0

ALIGNMENTS

```
RESULT 3
US-07-903-079B-2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      US-08-278-091-5
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           g
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ò
                                                                          ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ö
                                                                            Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Gaps
                                                                          ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ö
                                                                                                                                                                                                                 US-08-480-993-2

Sequence 2, Application US/08480993

Fatent No. 5721115

### PERENT No. 5721115

APPLICANT: Samuel, James E.

APPLICANT: Samuel, James E.

TITLE OF INVENTION: ADHESIN-OLIGOSACCHARIDE CONJUGATE

TITLE OF INVENTION: VACCINE FOR HAEMOPHILUS INFLUENZAE

NUMBER OF SEQUENCES:

CORRESPONDENCE ADDRESS:

ADDRESSEE: Pennie & Edmonds
                                      Score 12; DB 1; Length 463;
Pred. No. 0.00067;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        3.1%; Score 12; DB 1; Length 463; 100.0%; Pred. No. 0.00067; Live 0; Mismatches 0; Indels
                                                                          0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/480,993
FILING DATE: 07-JUN-1995
CLASSIFICATION: 435
                                                                       Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 PRICR APPLICATION DATA:
APPLICATION NUMBER: US 07/903,079
FILING DATE: 22-UNI-1992
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/810,966
FILING DATE: 20-DEC-1991
PROOR APPLICATION DATA:
APPLICATION NUMBER: US 07/631,698
FILING DATE: 21-DEC-1990
ATTORNEY/AGENT INFORMATION:
NAME: MASTOCK, S. Leslie
REGISTRATION NUMBER: 18,872
REERENEC/POCKET NUMBER: 7969-050
TELEPHONE: (212) 790-9090
TELEFAX: (212) 869-8864/9741
TELEFAX: (212) 869-8864/9741
TELEFAX: (514) PENNE
                                                                                                                                                                                                                                                                                                                                                                 ADDRESS:

ADDRESS:

ADDRESS:

AREET: 1155 Avenue of Americas
CITY: New York
COUNTRY: New York
COUNTRY: U.S.A.
ZIP: 10036
'OMPUTER PT'
MET.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  COMPUTER REALABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
                                  Query Match 3.1%; Scc
Best Local Similarity 100.0%; Pr
Matches 12; Conservative 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               LENGTH: 463 amino acids
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   unknown
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ; MOLECULE TYPE: protein US-08-480-993-2
                                                                                                                              114 TNNHVIDGADKI 125
                                                                                                         25 TNNHVIDGADKI 36
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    unknown
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Query Match
Best Local Similarity
Matches 12; Conserva
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  TNNHVIDGADKI 36
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              TYPE: amino acid
STRANDEDNESS: unl
US-08-485-569-2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  25
                                                                                                                                                                                                     RESULT 2
                                                                                                           ò
                                                                                                                                               a
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 q
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ò
```

```
ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Sequence 5, Application US/08278091
Patent No. 5506139
GENERAL INFORMATION:
GENERAL INFORMATION:
APPLICANT: LOOSMORE, Sheena M
APPLICANT: YANG, Yan-ping
APPLICANT: CHONG, Pele
APPLICANT: CHONG, Pele
APPLICANT: Michel H.
TITLE OF INVENTION: Analog of Haemophilus Hin47 Protein with
                                                                  APPLICANT: KITVAN, Howard C.
APPLICANT: Samuel, James E.
APPLICANT: Samuel, James E.
APPLICANT: No. 5843463berg, NIIS T.
TITLE OF INVENTION: ADHESIN-OLIGOSACCHARIDE CONJUGATE
TITLE OF INVENTION: VACCINE FOR HAEMOPHILUS INFLUENZAE
NUMBER OF SEQUENCES: 2
CORRESPONDENCE ADDRESS:
ADDRESSEE: Pennie & Edmonds
STREET: 1155 Avenue of Americas
CITY: New YORK
STATE: New YORK
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Length 463;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                    OPERATION SYSTEM: C-LOSS/MS-LOSS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/07/903,079B
FILING DATE: 22-JUN-1992
CLASSIFICATION: 435
PRIOR APPLICATION THER: US 07/810,966
FILING DATE: 20-DEC-1991
PRIOR APPLICATION DUMBER: US 07/810,696
FILING DATE: 20-DEC-1990
ATON NUMBER: US 07/631,698
FILING DATE: 21-DEC-1990
ATONENYAGENT INFORMATION:
NAME: MASTOCK S. Leslie
REGISTRATION NUMBER: 18,872
REFERENCE/DOCKET NUMBER: 18,872
REFERENCE/DOCKET NUMBER: 29090
TELEFRAX: (212) 790-9090
TELEFRAX: (212) 790-9090
TELEFRAX: (212) 869-8864/9741
TELEY: GALIA PENNIE
SEQUENCE CHARACTERISTICS:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       3.1%; Score 12; DB 2; Le
100.0%; Pred. No. 0.00067;
tive 0; Mismatches 0;
                                                                                                                                                                                                                                                                                                                                                                                                             MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
Sequence 2, Application US/07903079B Patent No. 5843463
GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       LENGTH: 463 amino acids
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Query Match 3.1
Best Local Similarity 100.
Matches 12; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       TOPOLOGY: unknown; MOLECULE TYPE: protein US-07-903-079B-2
                                                                                                                                                                                                                                                                                                                                                                                       COMPUTER READABLE FORM:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            NUMBER OF SEQUENCES: 2
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                25 TNNHVIDGADKI 36
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             amino acid
                                                                                                                                                                                                                                                                                                               New York
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 STRANDEDNESS:
                                                                                                                                                                                                                                                                                                                                      COUNTRY: UZIP: 10036
```

```
of Haemophilus Hin47 Protein with
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              APPLICANT: TANG, Yan-Ping
APPLICANT: YANG, Yan-Ping
APPLICANT: CHONG, Pele
APPLICANT: CHONG, Pele
APPLICANT: ONEN, Raymond P.
APPLICANT: NLIN, Michel H.
TITLE OF INVENTION: Analog of Haemophilus Hin47
TITLE OF INVENTION: Reduced Protease Activity
NUMBER OF SEQUENCES: 23
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              NAME: Stewart, Michael I.
REGISTRATION NUMBER: 24,973
REFERENCE/DOCKET NUMBER: 1038-493 MIS:VG
TELECOMMUNICATION INFORMATION:
TELEPRONE: (416) 595-1155
ITELEFAX: (416) 595-1163
INFORMATION FOR SEQ ID NO: 5:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    E: Sim & McBurney
Suite 701, 330 University Avenue
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Sequence 5, Application US/08472173 Patent No. 5665353 GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             LENGTH: 472 amino acids
                                                                                                                                                                                                                                     ; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
US-08-483-859-5
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             TYPE: amino acid
STRANDEDNESS: single
                                                                                                                                                                                                                                                                                                                                                                                                                                    160 GIGFAIPSNMVK 171
                                                                                                                                                                                                                                                                                                                                                                                                                                                          CITY: Toronto STATE: Ontario
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ADDRESSEE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    US-08-472-173-5
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            STREET:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                RESULT 6
                                                                                                                                                                                                                                                                                                                                                                                                                                                                            g
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ő
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  APPLICANT: LOOSMORE, Sheena M.
APPLICANT: LOOSMORE, Sheena M.
APPLICANT: TANG, Yan-Ping
APPLICANT: CHONG, Pele
APPLICANT: CHONG, Pele
APPLICANT: MICHEL H.
TITLE OF INVENTION: Analog of Haemophilus Hin47 Protein with
TITLE OF INVENTION: Reduced Protease Activity
NUMBER OF SEQUENCES: 23
CORRESPONDENCE ADDRESS:
ADDRESSEE: Sim & MCBURNEY
CITY: Toronto
STREET: Suite 701, 330 University Avenue
CITY: Toronto
STREET: Gondario
COUNTRY: Canada
ZIP: MSG 1R7
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ;
0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Length 472;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Indels
                                                        COUNTRY: Canada

ZIT: ILLIANG
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: TBM PC compatible
COMPUTER: PACHTING SYSTEM: TC compatible
CLASSIFICATION NUMBER: US/08/278,091
FILING DATE: 21-JUL-1994
CLASSIFICATION NUMBER: 24,973
REGISTRATION NUMBER: 24,973
REGISTRATION NUMBER: 1038-371
TELEFNORE: (416) 595-1155
TELEFNORE: (416) 595-1163
INFORMATION FOR SEQ ID NO: 5:
SEQUENCE CHARACTERISTICS:
LENGTH: 472 and no acids
LENGTH: 472 and no acids
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/483,859
FILING DATE: 07-JUN-1995
CLASSIFICATION: 435
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Query Match
3.1%; Score 12; DB 1; Le
Best Local Similarity 100.0%; Pred. No. 0.00068;
Adtches 12; Conservative 0; Mismatches 0;
ADDRESSEE: Sim & McBurney
STREET: Sulte 701, 330 University Avenue
CITY: Toronto
STATE: Ontario
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/296,149
FILING DATE: 26-AUG-1994
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/278,091
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               RESULT 5
US-08-483-859-5
US-08-480-65
Sequence 5, Application US/08483859
Patent No. 5656436
GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
US-08-278-091-5
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        160 GIGFAIPSNMVK 171
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              1111111111
263 GIGFAIPSNMVK 274
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Matches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     g
```

```
ö
                                                                                                                                                                                                                                                                                                                                                                           Gaps
                                                                                                                                                                                                                                                                                                                                                                        ;;
0
                                                                                                                                                                                                                                                                                                                             Length 472;
                                                                                                                                                                                                                                                                                                                                                                      0; Indels
                                                                                                                                                                                                                                                                                                                                Score 12; DB 1; L Pred. No. 0.00068;
                                  NAME: Stewart, Michael I.
REGISTRATION NUMBER: 24,973
REFERNCE/DOCKET NUMBER: 1038-495 MIS:V9
TELEPHONE: (416) 595-1155
TELEPHONE: (416) 595-1153
INFORMATION FOR SEQ ID NO: 5:
SEQUENCE CHARACTERISTICS:
LENGTH: 472 amino acids
                                                                                                                                                                                                                                                                                                                                Query Match 3.1%; Score 12; DB Best Local Similarity 100.0%; Pred. No. 0.0 Matches 12; Conservative 0; Mismatches
FILING DATE: 21-JUL-1994 ATTORNEY/AGENT INFORMATION:
```

```
Indels
                                                                                                                                                                                STREET: Suite 701, 330 University Avenue STREET: Suite 701, 330 University Avenue CITY: Tocnoto STATE: Ontario COUNTRY: Canada ZIP: MSG 1R7
COMPUTER: READABLE FORM: MEDIUM TYPE: Floppy disk COMPUTER: IBM PC COMPATION SYSTEM: PC-DOS/MS-DOS SOFTWATE: Patentin Release #1.0, Version #1.25 CURRENT APPLICATION NUMBER: US/08/482,816 FILING DATE: 07-JUN-1995 CLASSIFICATION: 435
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                3.1%; Score 12; DB 2; Lv
100.0%; Pred. No. 0.00068;
tive 0; Mismatches 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                    FILING DATE: 0/-0NW-1993
PRIOR APPLICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/296,149
FILING DATE: 26-AUG-1994
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/278,091
FILING DATE: 21-UUL-1994
ATTORNEY AGENT INFORMATION:
NAME: Stewart, Michael I
REGISTRATION NUMBER: 24,973
REFERENCE/DOCKET NUMBER: 1038-494 MIS:V9
TELEFORMUNICATION INFORMATION:
TELEFORMUNICATION INFORMATION:
TELEFORMUNICATION SEO. 1163
INFORMATION FOR SEO. ID NO: 5:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     LENGTH: 472 amino acids
TYPE: amino acid
STRANDEDNESS: single
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Query Match 3.1
Best Local Similarity 100.
Matches 12; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         160 GIGFAIPSNMVK 171
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ; TOPOLOGY: 11near
US-08-482-816-5
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Ontario
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    RESULT 9
US-08-296-149-5
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             STATE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           δλ
                                                                           ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ö
                                                                           Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Gaps
                                                                                                                                                                                                                                   Sequence 5, Application US/08487167

Patent No. 5865302

GENERAL INFORMATION:

APPLICANT: LOOSWORE, Sheena M.

APPLICANT: TANG, Yan-Ping

APPLICANT: CHONG, Pele

APPLICANT: CHONG, Pele

APPLICANT: CHONG, Pele

TITLE OF INVENTION: Analog of Haemophilus Hin47 Protein with

TITLE OF INVENTION: Reduced Protease Activity

NUMBER OF SEQUENCES: 23

CORRESPONDENCE ADDRESS:

ADDRESSEE: Sim & Medburney

STREET: Suite 701, 330 University Avenue
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ö
                                                                           ó;
                                   Query Match 3.1%; Score 12; DB 1; Length 472; Best Local Similarity 100.0%; Pred. No. 0.00068; Matches 12; Conservative 0; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          3.1%; Score 12; DB 2; Length 472; 100.0%; Pred. No. 0.00068; Pred. No. 0.10068; Ive 0; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               NAME: Stewart, Michael I.
REGISTRATION NUMBER: 24,973
REFERNE/POCKET NUMBER: 1038-508 MIS:vg
TELECOMMUNICATION INFORMATION:
TELEPHONE: (416) 595-1155
TELEFAX: (416) 595-1155
INFORMATION FOR SEQ ID NO: 5:
SEQUENCE CHARACTERISTICS:
LENGTH: 472 amino acids
TYPE: amino acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Query Match 3.1
Best Local Similarity 100.
Matches 12; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   STRANDEDNESS: single
TOPOLOGY: linear
                                                                                                                                  263 GIGFAIPSNMVK 274
                                                                                                           160 GIGFAIPSNMVK 171
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 160 GIGFAIPSNMVK 171
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     COUNTRY: Canada
ZIP: M5G 1R7
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                STATE: Ontario
COUNTRY: Canada
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Toronto
US-08-472-173-5
                                                                                                                                                                                                                     US-08-487-167-5
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        US-08-487-167-5
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         RESULT 8
                                                                                                             ò
                                                                                                                                             g
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   g
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ò
```

```
Patent No. 5935573
GENERAL INFORMATION:
APPLICANT: LOOSMONE, Sheena M
APPLICANT: ANG, Yan-Ping
APPLICANT: CHONG, Pele
APPLICANT: CHONG, Pele
APPLICANT: KLEIN, Michel H.
TITLE OF INVENTION: Analog of Haemophilus Hin47 Protein with Reduced Protease A
NUMBER OF SEQUENCES: 23
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   sequence 5. Application US/08296149
sequence 5. Application US/08296149
sequence 5. Application US/08296149
sequence 5. Application US/08296149
sequence 5. Application US/08296149
sequence 6. Sequence 5. Seena M
septicant: Looswork. Sheena M
septicant: CGNOK, Pale
septicant: CGNOK, Pale
septicant: CHONG, Pale
septicant: Misself 6. Sequence 7. Sequence 7. Sequence 8. Sequence 9. Sequence 9. Sequence 8. Sequence 9. S
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Length 472;
```

```
ö
                                                                                                                                                                                                                                                                                                                                                                 ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Gaps
                                                                                                                                                                                                                                                                                                                                                                 Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ;
0
                                                                                                                                                                                                                                                                                                                                                                 ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       TITLE OF INVENTION: ANALOG OF HAEMOPHILUS HIN47 WITH REDUCED TITLE OF INVENTION: PROTEASE ACTIVITY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Query Match 3.1%; Score 12; DB 2; Length 472; Best Local Similarity 100.0%; Pred. No. 0.00068; Matches 12; Conservative 0; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                       Length 472;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         STRUCT
CITY: TOTOLL
STATE: Ontario
COUNTRY: Canad:
ZIP: M5G 1R7
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC Compatible
COMPUTER: PACENTIN PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/615,271
FTLING APPLICATION: 514
                                                                                                                                                                                                                                                                                                                   3.1%; Score 12; DB 2; Lv
100.0%; Pred. No. 0.00068;
tive 0; Mismatches 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ADDRESSEE: Sim & McBurney
STREET: 6th Floor, 330 University Avenue
                                                    1038-671 MIS:jb
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        US-08-615-271-5
Sequence 5, Application US/08615271
Patent No. 5981503
GENERAL INFORMATION:
APPLICANT: LOOSMORE, Sheena M.
APPLICANT: CHONG, Pele
NAME: Stewart, MILLS REGISTRATION NUMBER: 24,973
REFERENCE/POCKER'N NUMBER: 1038
TELECOMUNICATION INFORMATION:
TELEPHONE: (416,595-1155
TELEPHONE: (416,595-1163
INFORMATION FOR SEQ ID NO: 5:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        FILING DATE: 20-JUN-1996
CLASSIFICATION: 514
ATTORREY/AGENT INNORMATION:
NAME: Stewart, Michael I
REGISTRATION NUMBER: 24,973
REPERENCE/DOCKEY
TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 TELEPHONE: (416) 595-1155
TELEFAX: (416) 595-1163
INFORMATION FOR SEQ ID NO: 5:
                                                                                                                                                                                  LENGTH: 472 amino acids
TYPE: amino acid
STRANDEDNESS: single
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           LENGTH: 472 amino acids
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    NUMBER OF SEQUENCISS: 23
CORRESPONDENCE ADDRESS:
ADDRESSEE: Sim & McBur
                                                                                                                                                                                                                                                                                                                                                              Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             TYPE: amino acid
STRANDEDNESS: single
                                                                                                                                                                                                                                                                                                                                                                                                            160 GIGFAIPSNMVK 171
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  160 GIGFAIPSNMVK 171
                                                                                                                                                                                                                                                                                                                                                                                                                                      Best Local Similarity
Matches 12; Consenve
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ; TOPOLOGY: linear US-08-615-271-5
                                                                                                                                                                                                                                                         linear
                                                                                                                                                                                                                                                         ;
US-08-801-499-5
                                                                                                                                                                                                                                                                                                                          Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        RESULT 11
                                                                                                                                                                                                                                                                                                                                                                                                                                                      QQ
                                                                                                                                                                                                                                                                                                                                                                                                                 ŏ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              APPLICANT: LOOSMORE, Sheena M
APPLICANT: YANG, Yan-Ping
APPLICANT: CHONG, Pele
APPLICANT: COMEN, Raymond P.
APPLICANT: KLEIN, Michel H.
APPLICANT: KLEIN, Michel H.
NUMBER OF SEQUENCES: 23
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ;
0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ;
0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    3.1%; Score 12; DB 2; Length 472; 100.0%; Pred. No. 0.00068; tive 0; Mismatches 0; Indels
                                                                  MEDIUM TYPE: RIOPPY disk
COMPUTER: IBM PC compatible
COMPUTER: IBM PC compatible
COMPUTER: IBM PC compatible
COMPUTER: IBM PC compatible
COMPUTER: Patentin Release #1.0, Version #1.25
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/296,149
FILING DATE:
CLASSIFICATION: 514
ATTORNEY/AGENT INFORMATION:
NAME: SEEWART, Michael I
REGISTRATION NUMBER: 1038-390
TELECOMMUNICATION INFORMATION:
TELEPHONE: (416) 595-1155
TELEPHONE: (416) 595-1163
INFORMATION FOR SEQ ID NO: 5:
SEQUENCE CHARACTERISTICS:
LENGTH: 472 amino acids
TYPE: AMINOPARENT SINGLE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          STREET: 6th Floor, 330 University Avenue STREET: 6th Floor, 330 University Avenue STREET: 6th Floor, 330 University Avenue STATE: Ontario COUNTRY: Canada ZIP: M5G 1R7
COMPUTER READBLE FORM: MEDIUM TYPE: Floppy disk COMPUTER: IBM PC compatible OPERATING SYSTEM: PC-DOS/MS-DOS SOFTWARE: PAtentin Release #1.0, Version #1.25 CURRENT APPLICATION DATA: APPLICATION NUMBER: US/08/801,499
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      CLASSIFICATION: 514

PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/482,816
FILING DATE: 07-UN-1995
PRIOR APPLICATION NUMBER: US 08/296,149
FILING DATE: 26-AUG-1994
FILING DATE: 26-AUG-1994
FILING DATE: 21-UL-1994
APPLICATION NUMBER: US 08/278,091
FILING DATE: 21-UL-1994
ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       US-08-801-499-5
Sequence 5, Application US/08801499
Patent No. 5962430
GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Query Match 3.1
Best Local Similarity 100.
Matches 12; Conservative
                           ZIP: M5G IR7
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        CORRESPONDENCE ADDRESS:
ADDRESSEE: Sim & MCB
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      160 GIGFAIPSNMVK 171
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ; TOPOLOGY: linear
US-08-296-149-5
             Canada
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           FILING DATE:
           COUNTRY:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      g
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ò
```

a

```
GENERAL INFORMATION:
GENERAL INFORMATION:
APPLICANT: LOOSWORE, Sheena M.
APPLICANT: CHONG, Pele
APPLICANT: CHONG, Pele
APPLICANT: CHONG, Pele
TITLE OF INVENTION: ANALOG OF HAEMOPHILUS HIN47 WITH REDUCED
TITLE OF INVENTION: PROTEASE ACTIVITY
NUMBER OF SEQUENCES: 23
CORRESPONDENCE ADDRESS:
ADDRESSEE: sim & MCBURNEY
STREET: 6th Floor, 330 University Avenue
CITY: Toronto
                                                                                                              Analog of Haemophilus Hin47 Protein with
Reduced Protease Activity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Length 472;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Indels
                                                                                                                                                                                                                                                                                                            CITY: TOTORICO
STATE: Ontario
SCHAR: Canada
ZIP: M5G 1R7
COMPUTER READBLE FORM:
MEDIUM TYPE: FLOPPY disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PATENTIN Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/074,659
FILING DATE: O7-UN-1995
FILING DATE: O7-UN-1995
PRIOR APPLICATION NUMBER: US 08/487,167
FILING DATE: O7-UN-1995
PRIOR APPLICATION NUMBER: US 08/296,149
FILING DATE: 26-AUG-1994
PRIOR APPLICATION NUMBER: 105 08/278,091
FILING DATE: 21-UUL-1994
ATTORNEY/AGENT INFORMATION:
NAME: Stewart, Michael 1.
REGISTRATION NUMBER: 24,973
REFERENCE/DOCKET NUMBER: 1038-730 MIS:jb
TELEPHONE: (416) 595-1165
TELEPHONE: (416) 595-1165
TELEPHONE: CHARACTERISTICS:
SEQUENCE CHARACTERISTICS:
SEQUENCE CHARACTERISTICS:
CMMDIT OF THE COMPANION OF THE CHARACTERISTICS:
CMDIT OF THE COMPANION OF 
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Query Match
3.1%; Score 12; DB 3; La
Best Local Similarity 100.0%; Pred. No. 0.00068;
Matches 12; Conservative 0; Mismatches 0;
APPLICANT: OOMEN, Raymond P.
APPLICANT: KLEIN, Michel H.
TITLE OF INVENTION: Analog of Haemophilus H1
TITLE OF INVENTION: Reduced Protease Activit
NUMBER OF SEQUENCES: 23
CORRESPONDENCE ADDRESS:
ADDRESSEE: Sim & McBurney
STREET: 6th Floor, 330 University Avenue
CITY: Toronto
STATE: Ontario
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Sequence 5, Application US/09106468 Patent No. 6114125
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      TYPE: amino acid
STRANDEDNESS: single
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               160 GIGFAIPSNMVK 171
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     linear
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Canada
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ;
US-09-074-659-5
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       COUNTRY:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    RESULT 14
US-09-106-468-5
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ð
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        q
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ;
0
                                                                                                                                                                                                                                                                                            APPLICANT: LOGSMORE, Sheena M.
APPLICANT: YANG, Yan-Ping
APPLICANT: CHONG, Pele
APPLICANT: COMEN, Raymond P.
APPLICANT: KLEIN, Michel H.
TITLE OF INVENTION: Analog of Haemophilus Hin47 Protein with
TITLE OF INVENTION: Reduced Protease Activity
CORRESPONDENCE 23
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          3.1%; Score 12; DB 3; Length 472; 100.0%; Pred. No. 0.00068; tive 0; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/074,660
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ADDRESSEE: Sim & McBurney
STREET: 6th Floor, 330 University Avenue
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        1038-731 MIS:jb
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                FILING DATE:

CLASSIFICATION:

PRIOR APPLICATION DATA:

APPLICATION NUMBER: US 08/487,167

FILING DATE: 07-JUN-1995

PRIOR APPLICATION NUMBER: US 08/296,149

FILING DATE: 26-AUG-1994

PRIOR APPLICATION NUMBER: US 08/278,091

FILING DATE: 21-JUL-1994

ATORNEY-AGENT INFORMATION:

NAME: SLEWART, Michael I.

REGISTRATION NUMBER: 24,973

REFERENCE/POCKET NUMBER: 1038-731 M.

TELECOMMUNICATION INFORMATION:

TELECOMMUNICATION INFORMATION:

TELECOMMUNICATION INFORMATION:

TELECOMMUNICATION INFORMATION:

TELECOMMUNICATION INFORMATION:

TELECOMMUNICATION INFORMATION:

SEQUENCE: (416) 595-1163

INFORMATION FOR SEQ ID NO: 5:

SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         US-09-074-659-5

; Sequence 5, Application US/09074659

; Patent No. 6025342

; GENERAL INFORMATION:

; APPLICANT: LOCSMORE, Sheena M.

; APPLICANT: YANG, Yan-Ping

; APPLICANT: CHONG, Pele
                                                                                                                                           RESULT 12
US-09-074-660-5
Sequence 5, Application US/09074660
Patent No. 6020183
GENERAL INFORMATION:
APPLICANT: LOOSMORE, Sheena M. APPLICANT: YANG, Yan-Ping
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 CITY: Toronto
STATE: Ontario
COUNTY: Canada
ZIP: M5G 1R7
COMPUTER READABLE FORM:
MEDIUM IYPE: Floppy di
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Query Match 3.1
Best Local Similarity 100.
Matches 12; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  TYPE: amino acid
STRANDEDNESS: single
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               160 GIGFAIPSNMVK 171
                                                     263 GIGFAIPSNMVK 274
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 1614111111
263 GIGFAIPSNMVK 274
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              TOPOLOGY: 11near
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          FILING DATE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   RESULT 13
```

ö

Gaps

ö

å g

```
ŏ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   g
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Sequence 5, Application US/09106466A

Patent No. 6447057

CENERAL INCOMENTE, Sheena M.
APPLICANT: CANG, Yan-Ping
APPLICANT: CHONG, Pele
APPLICANT: CHONG, Pele
APPLICANT: CHONG, Pele
TITLE OF INVENTION: ANALOG OF HAEMOPHILUS HIN47 WITH REDUCED
TITLE OF INVENTION: PROTEASE ACTIVITY
NUMBER OF SEQUENCES.3
CORRESPONDENCE ADDRESS:
ADDRESSEE: Sim & McBurney
STREET: 6th Floor, 330 University Avenue
CITY: Toronto
STREET: Ontario
STREET: Ontario
STREET: ADDRESS:
ADDRESSEE: Sim & McBurney
STREET: Ontario
STREET: Ontario
STREET: ADDRESSEE
STREET: ADDRESSEE
STREET: ADDRESSEE
STREET: CANGRAINES
STREET: ADDRESSEE

                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                3.1%; Score 12; DB 3; Length 472; 100.0%; Pred. No. 0.00068; tive 0; Mismatches 0; Indels
COMPUTER REALABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PATENTIN Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/106,468
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        SOFTWARE: Patentin Release #1.0, Version #1.30 CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/106,466A
                                                                                                                                                                                                                                                                                                                       CLASSIFCATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/615,271
FILING DATE: 20-JUN-1996
CLASSIFICATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     1038-825
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/615,271
FILING DATE: 20-JUN-1996
CLASSIFICATION: 514514
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ATTORNEY/AGENT INFORMATION:
NAME: Stewart, Michael I
REGISTRATION NUMBER: 24,973
REFERENCE/DOCKET NUMBER: 1038-
FELECOMMUNICATION INFORMATION:
FELECOMMUNICATION INFORMATION:
FELEFAX: (416) 595-1155
FELEFAX: (416) 595-1163
INFORMATION FOR SEQ ID NO: 5:
SEQUENCE CHARACTICS:
LENGTH: 472 amino acids
TYPE: amino acid
TYPE: amino acid
STRANDEDNESS: single
US-09-106-468-5
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ATTORNEY/AGENT INFORMATION: NAME: Stewart, Michael I
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                CLASSIFICATION: 514514
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Query Match 3.17
Best Local Similarity 100.
Matches 12; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    11111111111
263 GIGFAIPSNMVK 274
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         160 GIGFAIPSNMVK 171
                                                                                                                                                                                                                                                                                                              FILING DATE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     FILING DATE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                RESULT 15
US-09-106-466A-5
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         å
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              g
```

ö

· • ; •

```
AAW98445
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Chlamydia pneumoni
Escherichia coli s
S. typhimurium Htr
Lawsonia intracell
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Protein encoded by
Expressed antigen
Protein encoded by
Protein involved i
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               H. pylori GHPO 536
Antigen 1 from clu
                                                                                                 (without alignments)
1322.256 Million cell updates/sec
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.
                                                                                                                                                                                                                                                                                                                                                                                                       / SIDS2/gcddata/geneseqp-embl/AA1980.DAT:*
/ SIDS2/gcddata/geneseqp-embl/AA1981.DAT:*
/ SIDS2/gcddata/geneseq/geneseqp-embl/AA1981.DAT:*
/ SIDS2/gcddata/geneseqy-embl/AA1981.DAT:*
/ SIDS2/gcddata/geneseqy-embl/AA1981.DAT:*
/ SIDS2/gcddata/geneseqy-embl/AA1984.DAT:*
/ SIDS2/gcddata/geneseqy-embl/AA1984.DAT:*
/ SIDS2/gcddata/geneseqy-embl/AA1986.DAT:*
/ SIDS2/gcddata/geneseqy-embl/AA1986.DAT:*
/ SIDS2/gcddata/geneseqy-embl/AA1989.DAT:*
/ SIDS2/gcddata/geneseqy-embl/AA1989.DAT:*
/ SIDS2/gcddata/geneseqy-embl/AA1999.DAT:*
/ SIDS2/gcddata/geneseqy-embl/AA1991.DAT:*
/ SIDS2/gcddata/geneseqy-embl/AA1991.DAT:*
/ SIDS2/gcddata/geneseqy-embl/AA1992.DAT:*
/ SIDS2/gcddata/geneseqy-embl/AA1992.DAT:*
/ SIDS2/gcddata/geneseqy-embl/AA1992.DAT:*
                                                                                                                                                                   1 MIPKERMERALGSGVIISKD.......RPKRFLVLDLNQGYRIILVK 387
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            .DAT:*
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            /SIDS2/gcgdata/geneseg/genesegp-embl/AA2000.DAT:*/SIDS2/gcgdata/geneseg/genesegp-embl/AA2001.DAT:*/SIDS2/gcgdata/geneseg/genesegp-embl/AA2002.DAT:*
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Description
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        DAT:
                                                                                 November 18, 2002, 11:19:35; Search time 39 Seconds
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          /SIDS2/gcgdata/geneseq/genesegp-emb1/AA1994./SIDS2/gcgdata/geneseg/genesegp-emb1/AA1995.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        /SIDS2/gcgdata/geneseq/geneseqp-emb1/AA1996.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               /SIDS2/gcgdata/geneseq/geneseqp-emb1/AA1999.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  /SIDS2/gcgdata/geneseg/genesegp-emb1/AA1998
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   /SIDS2/gcgdata/geneseq/geneseqp-embl/AA1997
                                                                                                                                                                                                                                                                    908470
GenCore version 5.1.3 Copyright (c) 1993 - 2002 Compugen Ltd
                                                                                                                                                                                                                                                                 Total number of hits satisfying chosen parameters:
                                                                                                                                                                                                                                       908470 seqs, 133250620 residues
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            SUMMARIES
                                                                                                                                                                                                                                                                                                                                      Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

    protein search, using sw model

                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              AAW56771
AAR14625
AAG78605
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         AAW89977
AAW89984
AAW89817
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    AAY37309
ABB90581
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 AAW98445
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              AAW89850
                                                                                                                                                                                              BLOSUM62
Gapop 10.0 , Gapext 0.5
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     a
                                                                                                                                                                                                                                                                                                                                                                                             A_Geneseq_101002:*
                                                                                                                                       US-09-895-913A-120
                                                                                                                                                                                                                                                                                              seq length: 0 seq length: 2000000000
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  DB
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        $
Query
Match Length D
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            443
187
187
4491
475
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         74.4
46.9
38.7
37.3
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 0,00,7
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               100
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      749.5
722.5
718.5
714.5
                                                                                                                                        Title:
Perfect score:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        1441 909
                                                                                                                                                                                                Scoring table:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              1934
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Score
                                                        OM protein
                                                                                                                                                                                                                                                                                              Minimum DB
Maximum DB
                                                                                                                                                                    Sequence:
                                                                                                                                                                                                                                         Searched:
                                                                                                                                                                                                                                                                                                                                                                                               Database
                                                                                   Run on:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              2 4 4 5 9 7 8 9 0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Result
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Š.
```

```
BASBOll protein se
BASBOll protein se
BASBOll protein se
Protein encoded by
H. influenzae SB33
Haemophilus influe
                                                                                 Neisseria meningit
NGSP polypeptide o
NGSP polypeptide o
Staphylococcus epi
S. epidermidis ope
Neisseria meningit
                        Haemophilus influe
Haemophilus influe
Haemophilus influe
                                    Haemophilus influe
E. coli growth and
                                                Neisseria meningit
Neisseria meningit
Neisseria meningit
                                                             Neisseria meningit
Neisseria meningit
Neisseria meningit
                                                                         Neisseria gonorrhe
Neisseria meningit
                                             protein
                                                                                                           growth and
                                                                                                              Propionibacterium
Listeria monocytog
                                                                                                                           Group B Streptococ
Herbicidally activ
                                                                                                                                   Streptococcus poly
Streptococcus poly
                                                                                                                      Chlamydia pneumon
                                                                                                                                           Streptococcus
                                            Heat shock
                                                                                                           E. coli
                                                                                     AAY83151
AAY83150
ABP40266
AAG82365
                                                                AAY70409
AAY75750
                                                                                                      AAY52996
                                     AAB11835
                                                                         AAY75748
                                                                                                                                       ABP29849
                                                                                                                                           ABP30135
                                                                                  AAY70413
                                                                                                                                  ABP27963
                                                     AAY52994
584.5
584.5
559.5
536.5
536.5
528
528
528
520
520
54
74.5
74.5
```

ALIGNMENTS

```
GHPO protein; Helicobacter infection; gastroduodenal disease; gastritis; peptic ulcer disease.
                                                                                                                                                                                                                                                                                                                                                                                                                                                              ij
                                                                                                                                                                                                                                                                                                                                                                                                                                                                Tomb
                                                                                                                                                                                                                                                                                                                                                                                                                                                              RP,
                                                                                                                                                                                                                                                                                                                                                                                                                             (INMR ) MERIEUX OHAVAX PASTEUR MERIEUX SERUMS.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                Oomen
                                                                                                                                                                                                                                                                                                                                                                                                                                                              Miller C,
AAW98445 standard; Protein; 387 AA
                                                                                                                                                                                                                                                                                                                                    97ts-0902615.
97ts-0833457.
97ts-0881227.
                                                                                                                                                                                                                                                                                                                                                                                                           (HUMA-) HUMAN GENOME SCI INC
                                                                                                                                                                                                                                                                                                                                                                                                                                                              Kleanthous H,
                                                                                                                                                                                                                                                                                                    98WO-US06371
                                                                                                       H. pylori GHPO 53% protein
                                                                    31-MAR-1999 (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             WPI; 1998-542293/46.
N-PSDB; AAX14164..
                                                                                                                                                                                            Helicobacter pylori.
                                                                                                                                                                                                                                                                                                                                                                                                                                                              Al-Garawi A,
                                                                                                                                                                                                                                                                                                    01-APR-1998;
                                                                                                                                                                                                                                                                                                                                                      01-APR-1997;
24-JUN-1997;
                                                                                                                                                                                                                             WO9843478-A1
                                                                                                                                                                                                                                                                                                                                      29-JUL-1997;
                                                                                                                                                                                                                                                                 08-OCT-1998
                                    AAW98445;
```

Claim

FFFXXXX0000000XX

Matches _

ò g 19 61 121

g

ò g ö g ò

181 181 301

à

a

å

qq

361

RESULT 2 AAW89850

```
The present sequence represents a Helicobacter pylori antigenic protein that is characterised by immunoreactivity with H. pylori-positive antisera. The proteins are highly immunogenic and induce a long-lasting immune response that persists even after antimicriobial treatment. In antibody-detection assays, on sera, plasma, urine, saliva etc., they are highly sensitive and specific. The specification also describes 69 previously unrecognised immunogenic cluster families. H. pylori antigens are used to detect H. pylori-specific antibodies, for diagnosing infection or to confirm eradication of infection, and in vaccines to protect against H. pylori infection and related diseases (gastritis, peptic ulcer, gastric adenocarcinoma/lymphoma).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    57 MIPKERMERALGSGVIISKDGYIVTNNHVIDGADKIKVTIPGSNKEYSATLVGTDSESDL 116
                                                                                                               New Helicobacter pylori antigens and related nucleic acid sequences - useful in serological diagnosis and protective vaccines, providing
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Antigen; immunogenic cluster family; vaccine; gastritis; diagnosis; peptic ulcer; gastric adenocarcinoma; gastric lymphoma.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           1 MIPKERMERALGSGVIISKDGYIVTNNHVIDGADKIKVTIPGSNKEYSATLVGTDSESDL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          AVIRITKDNLPTIKFSDSNDISVGDLVFAIGNPFGVGESVTQGIVSALNKSGIGINSYEN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               FIQTDASINPGNSGGALIDSRGGLVGINTAIISKTGGNHGIGFAIPSNMVKDTVTQLIKT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 GKIERGYLGVGLQDLSGDLQNSYDNKEGAVVISVEKDSPAKKAGILVWDLITEVNGKKVK
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           GKIERGYLGVGLQDLSGDLQNSYDNKEGAVVISVEKDSPAKKAGILVWDLITEVNGKKVK
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               NTNELRNLIGSMLPNQRVTLKVIRDKKERAFTLTLAERKNPNKKETISAQNGAQGQLNGL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 QVEDLTQETKRSMRLSDDVQGVLVSQVNENSPAEQAGFRQGNIITKIEEVEVKSVADFNH
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Score 1934; DB 20;
Pred. No. 9.7e-149;
1; Mismatches 0;
                                          CP;
                                                                                                                                                                                        Claim 1; Page 211-212; 402pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            McAtee
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Ā
       (GENE-) GENELABS TECHNOLOGIES INC.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          AAW89977 standard; Protein; 451
                                                                                                                                                     long-lasting immune response
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Query Match 99.8%;
Best Local Similarity 99.7%;
Matches 386; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Protein encoded by clone b8.
                                          Lim MY,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Helicobacter pylori.
                                                                            WPI; 1999-009433/01
                                                                                                                                                                                                                                                                                                                                                                                                                                                     443 AA;
                                          Fry KE,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 18-FEB-1999
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               AAW89977;
                                                                                                                                                                                                                                                                                                                                                                                                                                                       Sequence
                                          Chow TP,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           117
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      181
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                297
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               121
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           237
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               241
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      301
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        RESULT 3
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           AAW89977
     g
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       qq
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       g
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         g
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              g
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ò
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          à
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               à
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                g
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ò
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               à
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                a
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      à
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             à
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ö
                                                                                                         This sequence represents a Helicobacter pylori GHPO protein of the invention. The polypeptides can be used for preventing or treating Helicobacter infections, and gastroduodenal diseases associated with these infections, including acute, chronic, and atrophic gastritis, and peptic ulcer diseases, e.g. gastric and duodenal ulcers. They can also be used for the production of antibodies. The products can also be used for detection and diagnosis.
                                                                                                                                                                                                                                                                                                                                                                                                                                                  AVIRITKDNLPTIKFSDSNDISVGDLVFAIGNPFGVGESVTQGIVSALNKSGIGINSYEN 120
                                                                                                                                                                                                                                                                                                                                                                                                                                                                     180
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      240
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           300
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    360
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           FIQTDASINPGNSGGALIDSRGGLVGINTAIISKTGGNHGIGFAIPSNMVKDTVTQLIKT 180
New isolated Helicobacter polynucleotides - used to develop products for the diagnosis, prevention and treatment of Helicobacter infections and gastrointestinal diseases
                                                                                                                                                                                                                                                                                                                                        Gaps
                                                                                                                                                                                                                                                                                                                                                                                            1 MIPKERMERALGSGVIISKDGYIVTNNHVIDGADKIKVTIPGSNKEYSATLVGTDSESDL 60
                                                                                                                                                                                                                                                                                                                                                                           MIPKERMERALGSGVIISKDGYIVTNNHVIDGADKIKVTIPGSNKEYSATLVGTDSESDL 60
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Antigen; immunogenic cluster family; vaccine; gastritis; diagnosis; peptic ulcer; gastric adenocarcinoma; gastric lymphoma.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     GKIERGYLGVGLQDLSGDLQNSYDNKEGAVVISVEKDSPAKKAGILVWDLITEVNGKKVK
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   QVEDLTQETKRSMRLSDDVQGVLVSQVNENSPAEQAGFRQGNIITKIEEVEVKSVADFNH
                                                                                                                                                                                                                                                                                                                                        ö
                                                                                                                                                                                                                                                                                                Length 387;
                                                                                                                                                                                                                                                                                                                                        Indels
                                                                                                                                                                                                                                                                                                   DB 19;
                                                                                                                                                                                                                                                                                                                       3.8e-149;
                                                                                                                                                                                                                                                                                                                                          .;
0
                                                                                                                                                                                                                                                                                                  100.0%; Score 1938; 100.0%; Pred. No. 3.8
                                                                                                                                                                                                                                                                                                                                        Mismatches
                                                                       8; Page 769-771; 2054pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       361 ALEKYKGKPKRFLVLDLNQGYRIILVK 387
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Ą.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    AAW89850 standard; Protein; 443
                                                                                                                                                                                                                                                                                                                                      ;
0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     98WO-US08487
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        97US-0061958
97US-0045107
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Antigen 1 from cluster 04a
                                                                                                                                                                                                                                                                                                                                    387; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Helicobacter pylori.
                                                                                                                                                                                                                                                                                                                   Similarity
                                                                                                                                                                                                                                                               387 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            WO9849314-A2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      14-OCT-1997;
25-APR-1997;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           18-FEB-1999
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     27-APR-1998;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 05-NOV-1998
                                                                                                                                                                                                                                                               Seguence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      AAW89850;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Antigen;
                                                                                                                                                                                                                                                                                                  Query Match
                                                                                                                                                                                                                                                                                                                       Local
```

ö

Gaps 9

; 0

Length 443; Indels 240

296

356 360 416

Ą.

(first entry)

```
The present sequence represents a Helicobacter pylori antigenic protein that is character/sed by immunoreactivity with H. pylori-positive antisera. The proteins are highly immunogenic and induce a long-lasting immune response that persists even after antimicriobial treatment. In antibody-detection assays, on sera, plasma, urine, saliva etc., they are highly sensitive wind specific. The specification also describes 69 previously unrecognised immunogenic cluster families. H. pylori antigens are used to detect H. pylori-specific antibodies, for diagnosing infection or to confirm eradication of infection, and in vaccines to protect against H. pylori infection and related diseases (gastritis, peptic ulcer, gastrit adenocarcinoma/lymphoma).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Helicobacter pylori antigens and related nucleic acid sequences seful in serological diagnosis and protective vaccines, providing
                                                                                                                         Antigen; immunogenic cluster family; vaccine; gastritis; diagnosis;
                                                                                                                                          peptic ulcer; gastric adenocarcinoma; gastric lymphoma.
                                                                                     Expressed antigen for clone Y261A.
                                                                                                                                                                                                                                                                                                                                                                                (GENE-) GENELABS (FECHNOLOGIES INC.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Claim 16; Page 322-323; 402pp;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                long-lasting immune response
                                                                                                                                                                                                                                                                                                                                                                                                                                                    WPI; 1999-009433/01.
                                                                                                                                                                              Helicobacter pylori.
                                                                                                                                                                                                                 WO9849314-A2
                                                                                                                                                                                                                                                                                       27-APR-1998;
                                                                                                                                                                                                                                                                                                                         14-OCT-1997;
                                                   18-FEB-1999
                                                                                                                                                                                                                                                                                                                                            25-APR-1997;
                                                                                                                                                                                                                                                     05-NOV-1998
                 AAW89984;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                    Chow TP,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        280
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          181
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              340
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  220
g
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ò
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      g
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ò
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          g
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  à
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  g
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        δ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              δ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                g
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ö
                                                                                                                                                                                                                                                                                                                                                                                                           The present sequence represents a Helicobacter pylori antigenic protein that is characterised by immunoreactivity with H. pylori-positive antisers. The proteins are highly immunogenic and induce a long-lasting immune response that persists even after antimicriobial treatment. In antibody-detection assays, on sera, plasma, urine, sallva etc., they are highly sensitive and specific. The specification also describes 69 previously unrecognised immunogenic cluster families. H. pylori antigens are used to detect H. pylori-specific antibodies, for diagnosing infection or to confirm eradication of infection, and in vaccines to protect against H. pylori infection and related diseases (gastritis,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        AVIRITKDNLPTIKFSDSNDISVGDLVFAIGNPFGVGESVTQGIVSALNKSGIGINSYEN 120
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              121 FIQTDASINPGNSGGALIDSRGGLVGINTAIISKTGGNHGIGFAIPSNMVKDTVTQLIKT 180
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      GKIERGYLGVGLQDLSGDLQNSYDNKEGAVVISVEKDSPAKKAGILVWDLITEVNGKKVK 240
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            NTNELRNLIGSMLPNQRVTLKVIRDKKERAFTLTLAERKNPNKKETISAQNGAQGQLNGL 300
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  QVEDLTQETKRSMRLSDDVQGVLVSQVNENSPAEQAGFRQGNIITKIEEVEVKSVADFNH 360
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         244
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Gaps
                                                                                                                                                                                                                                                                                                       New Helicobacter pylori antigens and related nucleic acid sequences - useful in serological diagnosis and protective vaccines, providing long-lasting immune response
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    9
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 MIPKERMERALGSGVIISKDGYIVTNNHVIDGADKIKVTIPGSNKEYSATLVGTDSESDL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Length 451;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Score 1904; DB 20;
Pred. No. 2.7e-146;
2; Mismatches 4;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      peptic ulcer, gastric adenocarcinoma/lymphoma).
                                                                                                                                                                                                                                                                                                                                                                             Claim 15; Page 317-318; 402pp; English.
                                                                                                                                                                                                                 McAtee CP;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ALEKYKGKPKRFLVLDLNQGYRIILVK 387
                                                                                                                                                                              (GENE-) GENELABS TECHNOLOGIES INC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             98.2%;
98.4%;
                                                                                   98WO-US08487
                                                                                                                       97US-0061958
                                                                                                                                          97US-0045107
                                                                                                                                                                                                                 Fry KE, Lim MY,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Best Local Similarity 98.4
Matches 381; Conservative
                                                                                                                                                                                                                                                  WPI; 1999-009433/01.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      451 AA;
                                                                                                                                                                                                                                                                      N-PSDB; AAV90921
             WO9849314-A2
                                                                                   27-APR-1998;
                                                                                                                       14-OCT-1997;
                                                                                                                                        25-APR-1997;
                                                 05-NOV-1998
                                                                                                                                                                                                                Chow TP,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  185
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              305
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      365
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      245
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            241
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          361
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        61
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      181
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  301
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          425
```

d ά 셤 ò g δ g δ q ò g ŏ

ò

English.

CP;

Lim MY,

Fry KE,

98NO-US08487. 97US-0061958 971JS-0045107

```
ö
                                                                                                                                                                                                      61 GIGFAIPSNAVKPTVTQLIKTGKIERGYLGVGLQDLSGDLQNSYDNKEGAVVISVEKDSP 120
                                                                                                                                                                                                                                                                                                                                                                       240
                                                                                                            100 VTQGIVSALNKSGIGINSYENFIQTDASINPGNSGGALIDSRGGLVGINTAIISKTGGNH 159
                                                                       Gaps
                                                                                                                                              9
                                                                                                                             AKKAGILVWDLIT'EVNGKKVKNTNELRNLIGSMLPNQRVTLKVIRDKKERAFTLTLAERK
                                                                                                                                                                                                                                                                                                                                    NPNKKETISAQN@AQGQLNGLQVEDLTQETKRSMRLSDDVQGVLVSQVNENSPAEQAGFR
                                                                                                                                                                                   160 GIGFAIPSNMVKITVTQLIKTGKIERGYLGVGLQDLSGDLQNSYDNKEGAVVISVEKDSP
                                                                       ö
                                  Length 288;
                                                                                                                                                                                                                                                                                                                                                                                                                                 QGNIITKIEEVEVKSVADFNHALEKYKGKPKRFLVLDLNQGYRIILVK 387
                                                                       Indels
                                  74.4%; Score 1441; DB 20;
100.0%; Pred. No. 6.1e-109;
Live 0; Mismatches 0;
                                                    Best Local Similarity 100. Matches 288; Conservative
 288 AA;
Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                  241
```

AAW89984 standard; Protein; 288 AA.

RESULT 4 AAW89984 9

AAW89817;

AAW89817

05-NOV-1998

```
AAX36754-Y37949 are encoded by open reading frames (ORFs) of the genome of Chlamydia trachomatis (see AAZ01425). The polypeptides can be used as vaccines against Chlamydia trachomatis. Antisense and ribozyme sequences can also be used to control growth of the microorganism. Chlamydia trachomatis is responsible for a large number of diseases, e.g. eye diseases such as conventional trachoma, nonendemic trachoma, paratrachoma, and inclusion conjunctivitis; genital diseases such as nongonococcal uretritis, epidymitis, cervicitis, salpingitis, and venereal lymphogranulomatosis. The polypeptides of the invention may be of use in treating these diseases.
                                                                                                                                                           Vaccine; eye disease; conventional trachoma; nonendemic trachoma; paratrachoma; inclusion conjunctivitis; genital disease; perihepatitis; nongonococcal uretritis; epidymitis; cervicitis; salpingitis; bartholinitis; pneumopathy; venereal lymphogranulomatosis.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  IRITKDNLPTIKFSDSNDISVGDLVFAIGNPFGVGESVTQGIVSALNKSGIGINSYENFI 122
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           3 PKERMERALGSGVIISKDGYIVTNNHVIDGADKIKVTIPGSNKEYSATLVGTDSESDLAV
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          QTDASINPGNSGGALIDSRGGLVGINTAIISKTGGNHGIGFAIPSNMVKDTVTQLIKTGK
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               183 IERGYLGVGLQDLSGDLQNSY--DNKEGAVVISVEKDSPAKKAGILVWDLITEVNGKKVK
                                                                                                                   Protein involved in intermediate metabolism of polypeptides.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              38.7%; Score 749.5; DB 20;
41.5%; Pred. No. 2.1e-52;
tive 83; Mismatches 126;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Disclosure; Page 1044-1045; 1755pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Genome sequence of Chlamydia trachomatis
AAY37309 standard; Protein; 491 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                         97FR-0015041
97FR-0016034
                                                                                                                                                                                                                                                                                                                                                                                  98WO-IB01939
                                                                                                                                                                                                                                                                                                                                                                                                                         98US-0107077
                                                                              (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Best Local Similarity 41.5
Matches 162; Conservative
                                                                                                                                                                                                                                                            Chlamydia trachomatis
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  WPI; 1999-371125/31
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             491 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   (GEST ) GENSET
                                                                                                                                                                                                                                                                                                     W09928475-A2
                                                                                                                                                                                                                                                                                                                                                                                  27-NOV-1998;
                                                                                                                                                                                                                                                                                                                                                                                                                                                              17-DEC-1997;
                                                                                                                                                                                                                                                                                                                                                                                                                         04-NOV-1998;
                                                                                                                                                                                                                                                                                                                                                                                                                                              28-NOV-1997;
                                                                              07-0CT-1999
                                                                                                                                                                                                                                                                                                                                            10-JUN-1999
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Griffais R;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          123
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              63
  ò
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   q
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Q
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            g
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      a
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            á
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       δ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ÷
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                The present sequence represents a Helicobacter pylori antigenic protein that is characterised by immunoreactivity with H. pylori-positive antisers. The proteins are highly immunogenic and induce a long-lasting immuno response that persists even after antimicriobial treatment. In antibody-detection assays, on sera, plasma, urine, saliva etc., they highly sensitive and specific. The specification also describes 69 previously unrecognised immunogenic cluster families. H. pylori antigens are used to detect H. pylori-specific antibodies, for diagnosing infection or to confirm eradication of infection, and in vaccines to protect against H. pylori infection and related diseases (gastritis,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           LVSQVNENSPAEQAGFRQGNIITKIEEVEVKSVADFNHALEKYKGKPKRFLVLDLNQGYR 382
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       62
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              New Helicobacter pylori antigens and related nucleic acid sequences - useful in serological diagnosis and protective vaccines, providing
                                                                                                                                                                           Antigen; immunogenic cluster family; vaccine; gastritis; diagnosis; peptic ulcer; gastric adenocarcinoma; gastric lymphoma.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      263 IRDKKERAFTLTLAERKNPNKKETISAQNGAQGQLNGLQVEDLTQETKRSMRLSDDVQGV
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                203 YDNKEGAVVISVEKDSPAKKAGILVWDLITEVNGKKVKNTNELRNLIGSMLPNQRVTLKV
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Length 187;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            1; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Score 909; DB 20;
Pred. No. 5.6e-66;
2; Mismatches 1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       peptic ulcer, gastric adenocarcinoma/lymphoma).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Lim MY, McAtee CP;
              AAW89817 standard; Protein; 187 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Claim 15; Page 103; 402pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                          (GENE-) GENELABS TECHNOLOGIES INC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          5;
                                                                                                                                      7
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          long-lasting immune response
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     46.9%;
98.4%;
                                                                                                                                                                                                                                                                                                                                                             98WO-US08487
                                                                                                                                                                                                                                                                                                                                                                                                97US-0061958
97US-0045107
                                                                                               18-FEB-1999 (first entry)
                                                                                                                                      Protein encoded by clone
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Matches 182; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         WPI; 1999-009433/01.
                                                                                                                                                                                                                                     Helicobacter pylori
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Chow TP, Fry KE,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              187 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         N-PSDB; AAV90552.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              |||||
|ILVK 187
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       IILVK 387
                                                                                                                                                                                                                                                                              W09849314-A2
                                                                                                                                                                                                                                                                                                                                                           27-APR-1998;
                                                                                                                                                                                                                                                                                                                                                                                              14-OCT-1997;
                                                                                                                                                                                                                                                                                                                                                                                                                       25-APR-1997;
```

7:

Gaps 62

DB 20; Length 491;

Sequence Query Match 290

351 SLSALRNAISLAMPGTRVILKIVREGKTIEIPVTVTQ------IPTEDGVSALQKMG 401

241 NTNELRNLIGSMLPNQRVTLKVIRDKKERAFTLTLAERKNPNKKETISAQNGAQG-QLNG

183

RESULT 6

į

63 323 123 383

ò d ò g ò g ö Ŋ

7;

```
N-PSDB; AAV29528
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 13-OCT-1998
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 26-AUG-1997;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   06-SEP-1996;
25-OCT-1996;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        13-DEC-1996;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     EP828003-A2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            11-MAR-1998
                                                                                                      Matches 158;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Browne MJ,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           AAW56771;
                                                         Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Livi GP,
                                                                               Query Match
                                                                                           Best Local
                                                                                                                                                                                              162
                                                                                                                                                                                                                                                                                       282
                                                                                                                                                                       57
                                                                                                                                                                                                                                                                177
                                                                                                                                                                                                                                                                                                              235
                                                                                                                                                                                                                                                                                                                                                          295
                                                                                                                                                                                                                    117
                                                                                                                                                                                                                                                                                                                                                                                                                                                                          AAW5677
                                                                                                                                                                                                                                                                                                                                                                                                                                                                RESULT
  ប្រក្តប្តូន្ធន
                                                                                                                                                                                             qq
                                                                                                                                                                                                                                         g
                                                                                                                                                                                                                                                                                      g
                                                                                                                                                                                                                                                                                                                                 Op
                                                                                                                                                                                                                                                                                                                                                                                                                          g
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ò
                                                                                                                                                 g
                                                                                                                                                                       ŏ
                                                                                                                                                                                                                    ò
                                                                                                                                                                                                                                                                δ
                                                                                                                                                                                                                                                                                                              ò
                                                                                                                                                                                                                                                                                                                                                          Q
                                                                                                                                                                                                                                                                                                                                                                               g
                                                                                                                                                                                                                                                                                                                                                                                                       ò
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Sequences ABB90526-ABB90715 represent novel proteins from Chlamydia pneumoniae (strain CWL029), and ABL91184-ABL91373 represent DNA encoding them. The proteins are predicted to be immunogenic and may therefore be useful in vaccine production and for diagnostic purposes. Chlamydia pneumoniae is a common cause of respiratory disease in humans, and is also involved in the development of cardiovascular diseases such as atherosclerosis, coronary artery disease, carcolid artery stenosis, myocardial infarction, cerebrovascular disease, aortic aneurysm, claudication and stroke. The proteins and nucleic acids of the invention may be used in vaccines and pharmaceutical compositions for the prevention or treatment of chlamydial infections, particularly Chlamydia pneumoniae infections. The proteins may also be used in the detection of
                                                                                                                                                                                                                 Chlamydial infection; antigen; immunogen; vaccine; diagnosis; muman respiratory disease; cardiovascular disease; atherosclerosis; coronary artery disease; carcid artery stenosis; myocardial infarction; cerebrovascular disease; aortic aneurysm; claudication; stroke;
LQVEDLTQETKRSMRLSDDVQGVLVSQVNENSPAEQAGFRQGNIITKIEEVEVKSVADFN 359
             Novel Chlamydia pneumoniae protein useful in the manufacture of a medicament for treatment or prevention of infection due to Chlamydia, preferably Chlamydia pneumoniae, and for diagnostic purposes
                                                                                                                                                                                             Chlamydia pneumoniae cp7306 protein, SEQ ID NO:111
                                                         |: ||: |::| | |::|
QVLKNSKGEN---VLLMVSQGDVVRFIVLK 488
                                                                                                                                                                                                                                                                                                                                                         "Mature protein"
                                          HALEKYKGKPKRFLVLDLNQG--YRIILVK 387
                                                                                                                                                                                                                                                                                                                       1..20
/label= Signal_peptide
21..488
/note= "Mature protein"
                                                                                                                                                                                                                                                                                                            Location/Qualifiers
                                                                                                                         ABB90581 standard; Protein; 488 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Claim 1; Page 95; 364pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                           2000GB-0017047.
2000GB-0017983.
2000GB-0019368.
2000GB-0020440.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        2000GB-0022583.
2000GB-0027549.
2000GB-0031706.
                                                                                                                                                                                                                                                                                                                                                                                                                           2001WO-IB01445
                                                                                                                                                                       (first entry)
                                                                                                                                                                                                                                                                                      Chlamydia pneumoniae.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               WPI; 2002-154726/20.
N-PSDB; ABL91239.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Grandi G;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      (CHIR-) CHIRON SPA.
                                                                                                                                                                                                                                                                                                                                                                               WO200202606-A2
                                                                                                                                                                                                                                                               strain CWL029.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  07-AUG-2000;
18-AUG-2000;
14-SEP-2000;
10-NOV-2000;
                                                                                                                                                                                                                                                                                                                                                                                                                           03-JUL-2001;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                        21-JUL-2000;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                22-DEC-2000;
                                                                                                                                                                                                                                                                                                                                                                                                                                                  03-JUL-2000;
                                                                                                                                                                                                                                                                                                                                                                                                                                                            11-JUL-2000;
                                                                                                                                                                     29-JUL-2002
                                                                                                                                                                                                                                                                                                                                                                                                      10-JAN-2002
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Ratti G,
                                                                                                                                                 ABB90581;
                                                                                                                                                                                                                                                                                                                       Peptide
                                                                                                                                                                                                                                                                                                                                              Protein
                     402
                                                                  462
300
                                            360
                                                                                                               ABB90581
                                                                                                   RESULT
                                                                                                                                      셤
                                            ŏ
                                                                g
à
```

```
branched
                                                                                                                                                                                                                                                                                                                                                                                                              ESDLAVIRITKDNLPTIKFSDSNDISVGDLVFAIGNPFGVGESVTQGIVSALNKSGIGIN 116
                                                                                                                                                                                                                                                                                                                                    LIRDGQVTRGFL/3VTLQPIDAELAACYKLEKVYGALVTDVVKGSPADKAGLKQEDVIIAY 341
                                                                                                                                                                                                                                                  Gaps
                                                                                                                                                                                                                                                                                                     2 IPKER-----MERALGSGVIISKDGYIVTNNHVIDGADKIKVTIPGSNKEYSATLVGTDS 56
Chlamydia pneumoniae, and the nucleic acids may be used in PCR, bra bra by probe assay or blotting techniques for determining Chlamydia pneumoniae gene expression. The present sequence represents a specifically claimed Chlamydia pneumoniae protein of the invention
                                                                                                                                                                                                                                                                                                                                                                                                                                                 SYENFIQTDASINPGNSGALIDSRGGLVGINTAIISKTGGNHGIGFAIPSNMVKDTVTQ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       LIKTGKIERGYLJJVGLQDLSGDLQNSY - - DNKEGAVVISVEKDSPAKKAGILVWDLITEV
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             GOLNGLOVEDLT()ETKRSMRLSDDVQGVLVSQVNENSPAEQAGFRQGNIITKIEEVEVKS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                NGKKVKNTNELRNLIGSMLPNQRVTLKVIRDKKERAFTLTLAERKNPNKKETISAQNGAQ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     PS-1; presenilin; presenilin-1; PSP-1; Alzheimer's disease; htra; serine protease; neurodegeneration; predisposition; diagnosis.
                                                                                                                                                                                      37.3%; Score 722.5; DB 23; Length 488; 40.0%; Pred. No. 3.3e-50; ive 82; Mismatches 134; Indels 21;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       EH;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Karran
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      VADFNHALEKYKGKPKRFLVLDLNQG--YRIILVK 387
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         454 IEDLNRTL---KIJSNNENILLMVSQGDVIRFIALK
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Creasy CL,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Escherichia coli serine protease htrA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Ź
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            AAW56771 standard Protein; 491
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       (SMIK ) SMITHKLINE BEECHAM CORP (SMIK ) SMITHKLINE BEECHAM PLC.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Clinkenbeard HE,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    96ths-0025436.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       97EP-0306501
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          96tfs-0032875.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 96us-0027873
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         (first entry)
                                                                                                                                                                                                                                               Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Southan CD;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   WPI; 1998-161101/15.
                                                                                                                                                                                                                     Similarity
                                                                                                                                     488 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Escherichia coli.
```

```
22-OCT-1999;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          20-NOV-2001
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       26-JUN-2001
                                                                                                                               Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                          AAG78605;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      vaccine.
                                                                                                                                                                                                                   89
                                                                                                                                                                                                                                                                                                        292
                                                                                                                                                                                                                                                                                                                                          352
                                                                                                                                                                                                                                                                                       188
                                                                                                                                                                                                                                                                                                                         246
                                                                                                                                                                                                                                                                                                                                                                                                                                                AAG78605
ò
                                                                                                                                                                                                  g
                                                                                                                                                                                                                    ò
                                                                                                                                                                                                                                  g
                                                                                                                                                                                                                                                    ò
                                                                                                                                                                                                                                                                    q
                                                                                                                                                                                                                                                                                       à
                                                                                                                                                                                                                                                                                                     g
                                                                                                                                                                                                                                                                                                                         ŏ
                                                                                                                                                                                                                                                                                                                                         g
                                                                                                                                                                                                                                                                                                                                                            ô
                                                                                                                                                                                                                                                                                                                                                                          g
                                                                                                                                                                                                                                                                                                                                                                                             ò
                                                                                                                                                                                                                                                                                                                                                                                                             g
                                                                                                                                                                                                                                                                                                                                                                                                                                                                           6
                                                                                                                                            112 ALGSGVIIDADKGYVVTNNHVVDNATVIKVQL-SDGRKFDAKMVGKDPRSDIALIQIQNP 170
                                                                                                                                                                        187
                                                                                                                                                                                                          306 TQETKRSMRLSDDVQGVLVSQVNENSPAEQAGFRQGNIITKIEEVEVKSVADFNHALEKY 365
                                                                                                                                                                                                                                                                                                                DNLPTIKFSDSNDISVGDLVFAIGNPFGVGESVTQGIVSALNKSGIGINSYENFIQTDAS 127
                                                                                                             Gaps
                                                                                                                             10 ALGSGVIISKD-GYIVTNNHVIDGADKIKVTIPGSNKEYSATLVGTDSESDLAVIRI-TK 67
                                                                                                                                                                                                                                              INPGNSGGALIDSRGGLVGINTAIISKTGGNHGIGFAIPSNMVKDTVTQLIKTGKIERGY
                                                                                                                                                                                                                                   LGVGLQDLSGDLQNS - - YDNKEGAVVISVEKDSPAKKAGILVWDLITEVNGKKVKNTNEL
                                                                                                                                                                                                                                                                     RNLIGSMLPNQRVTLKVIRDKKERAFTLTLAERKNPNKKETISAQNGAQGQLNGLQVEDL
         for
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Chatfield SN;
                                                   nseq
                                                                                                             25;
       Nucleic acids encoding human serum protease protein(s) – used diagnosing pre-disposition to Alzheimer's disease, etc.
                                                                                            DB 19; Length 491;
                                                 The sequence is that of the serine protease htrA which was in the isolation of PSP1.
                                                                                           Query Match 37.1%; Score 718.5; DB 19; Length Best Local Similarity 43.2%; Pred. No. 7e-50; Matches 163; Conservative 73; Mismatches 116; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                        TnphoA mutagenesis; signal peptide; stress protein;
heat shock protein; degP.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Johnson KS,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Hormaeche CE,
                                Example 2; Page 28-29; 65pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                    AAR14625 standard; Protein; 475 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Salmonella typhimurium strain C5
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      (WELL ) WELLCOME FOUNDATION LTD
                                                                                                                                                                                                                                                                                                                                                                                                                                                       S. typhimurium HtrA protein
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     91WO-GB00484
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     90GB-0007194
                                                                                                                                                                                                                                                                                                                                        KGKPKRFLVLDLNQGYR 382
                                                                                                                                                                                                                                                                                                                                                    -SKPS-VLALNIQRGDR 467
                                                                                                                                                                                                                                                                                                                                                                                                                                      (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Dougan G, Charles IG,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     WPI; 1991-325215/44.
N-PSDB; AAQ14416.
                                                                          491 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    23-MAR-1991;
                                                                                                                                                                                                                                                                                                                                                                                                                                     14-JAN-1992
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    30-MAR-1990;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  WO9115572-A
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    17-0CT-1991
                                                                                                                                                                                                                                                                                                                                                                                                                     AAR14625;
                                                                            Sequence
                                                                                                                                                                                                 128
                                                                                                                                                                                                                                                    291
                                                                                                                                                                                                                                                                      246
                                                                                                                                                                                                                                                                                                                        400
                                                                                                                                                                                                                                                                                                                                         366
                                                                                                                                                                                                                                                                                                                                                         453
                                                                                                                                                              68
                                                                                                                                                                                                                                  188
                                                                                                                                                                                                                                                                                                                                                                                           AAR14625
ID AAR1
                                                                                                                                                                                                                                                                                                                                                                                   RESULT 9
g
                                                                                                                                                                                                                                                                                                                                                                                                             XXXXXX
                                                                                                                              õ
                                                                                                                                             g
                                                                                                                                                               à
                                                                                                                                                                              a
                                                                                                                                                                                                                                  õ
                                                                                                                                                                                                                                                   g
                                                                                                                                                                                                                                                                     ò
                                                                                                                                                                                                                                                                                     쉽
                                                                                                                                                                                                                                                                                                     ò
                                                                                                                                                                                                                                                                                                                                         õ
                                                                                                                                                                                                                                                                                                                                                        g
```

```
HtrA; PonA; HypC; YefW; ABC1; Omp100; Lawsonia intracellularis infection;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                245
                                                                                                             TriphoA mutagenesis was used in the mouse virulent S. typhimurium strain CS. Mutants were selected likely to harbour lesions in genes that have a signal peptide sequence, i.e. proteins likely to be targetted through a bacterial membrane. Isolation of the DNA flanking the TriphoA insertion identified the gene (hrA) that has been insertionally activated. Comparison of the translated protein sequence showed that it shared 88% homology with the sequence of the htrA product from E. coli.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            DNLPTIKFSDSNDISVGDLVFAIGNPFGVGESVTQGIVSALNKSGIGINSYENFIQTDAS 127
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 128 INPGNSGGALIDSRGGLVGINTAIISKTGGNHGIGFAIPSNMVKDTVTQLIKTGKIERGY 187
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      351
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       RNLIGSMLPNQRVTLKVIRDKKERAFTLTLAERKNPNKKETISAQNGAQGQLNGLQVEDL 305
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           10 ALGSGVII-SKDGYIVTNNHVIDGADKIKVTIPGSNKEYSATLVGTDSESDLAVIRI-TK 67
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              LGVGLQDLSGDLQNS--YDNKEGAVVISVEKDSPAKKAGILVWDLITEVNGKKVKNTNEL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          306 TQETKRSMRLSDDVQGVLVSQVNENSPAEQAGFRQGNIITKIEEVEVKSVADFNHALEKY
ģ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                             25;
Attenuated microorganism useful in live vaccines - attenuated mutation in DNA sequence encoding e.g. a heat shock protein
                                                                                                                                                                                                                                                                                                                                                                                                                   Length 475;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Indels
                                                                                                                                                                                                                                                                                                                                                                                                                   36.9%; Score 714.5; DB 12;
42.9%; Pred. No. 1.4e-49;
tive 75; Mismatches 114;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Lawsonia intracellularis protein SEQ ID NO: 7.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ¥.
                                                                            Disclosure; Fig 1; 28pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     474
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   AAG78605 standard; Protein;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     20-OCT-2000; 2000JP-0320736
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      99US-0160922
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Matches 161; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  || | | |: :|
454 -SKPS-VLALNIQRG 466
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Lawsonia intracellularis.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 366 KGKPKRFLVLDLNQG 380
                                                                                                                                                                                                                                                                                                                                                                                                                      Query Match
Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                     475 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                JP2001169787-A.
```

ģ

```
(SMIK ) SMITHKLINE BEECHAM BIOLOGICALS.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  98GB-0008720.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Moraxella catarrhalis
                                                                                                                                                                                                                                                                                                                                                                                                                                                       surgical techniques.
                                                                               WPI: 2000-062033/05
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              433 AA;
                                                                                                    N-PSDB; AAZ48700
                                                                                                                                                              by this bacteria
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       W09955871-A1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       20-APR-1999;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  23-APR-1998;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   10-MAR-2000
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  04-NOV-1999.
                                        Ruelle J;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          AAY59354;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       RESULT 12
AAY59354
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        11
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        71
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     131
                                                                                                                                           New
  P X X B X X B X X B X X B X X B X X B X X B X X B X X B X X B X X B X X B X X B X X B X X B X X B X X B X X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B X B 
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        οy
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             g
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            g
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           g
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ŏ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          qq
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       οy
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            셤
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ò
                                                                                                                                                                                                                                                                                                                                                                                           11;
                                                                                                                                                                             The present invention provides isolated polynucleotides encoding HtrA, PODA, HypC, LysS, YefW, ABC1 or Omp100 protein of Lawsonia intracellularis. The sequences can be used in vaccines for the prevention of Lawsonia intracellularis infection. The present sequence is a protein of the invention.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             BASB011; immune response; bacterial infection; middle ear infection;
bacterial adhesion; extracellular matrix protein; tissue damage; therapy.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            264
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        265 SRGWIGVTIQDVDTNTAKALGLSQAKGALVGSVVPGDPADKAGLKVGDIVTQADGKQIDS 324
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       SESTERATATERPESVVKLKVWRDGKSKDISITLGERKTTSSQKQ-SSPESEDGAL-GLS 382
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 358
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         TDASINPGNSGGALIDSRGGLVGINTAIISKTGGNHGIGFAIPSNMVKDTVTQLIKTGKI 183
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ERGYLGVGLQDLSGDLQNS--YDNKEGAVVISVEKDSPAKKAGILVWDLITEVNGKKVKN 241
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                TNELRNLIGSMLPNQRVTLKVIRDKKERAFTLTLAERKNPNKKETISAQNGAQGQLNGLQ 301
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 65 I-TKDNLPTIKFSDSNDISVGDLVFAIGNPFGVGESVTQGIVSALNKSGIGINSYENFIQ 123
                                                                               ಧ
                                                                                                                                                                                                                                                                                                                                                                                           Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                ERALGSGVIISKDGYIVTNNHVIDGADKIKVTIPG-SNKEYS--ATLVGTDSESDLAVIR 64
                                                                               Lawsonia intracellularis polynucleotide and encoded protein, used prevent Lawsonia intracellularis infection -
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           VEDLTQETKRSMRLSDDVQ---GVLVSQVNENSPAEQAGFRQGNIITKIEEVEVKSVADF
                                                                                                                                                                                                                                                                                                                                                                                         22;
                                                                                                                                                                                                                                                                                                                                                Length 474;
                                                                                                                                                                                                                                                                                                                                                                                         Indels
                                                                                                                                                                                                                                                                                                                                              Query Match 35.3%; Score 684; DB 22; Best Local Similarity 43.3%; Pred. No. 4.2e-47; Matches 161; Conservative 70; Mismatches 119;
                                                                                                                                         Claim 12; Page 47-49; 67pp; Japanese.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            AAY59353 standard; Protein; 433 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      protein sequence #1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     99WO-EP02764
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            98GB-0008720
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              (first entry)
(PFIZ ) PFIZER PROD INC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Moraxella catarrhalis
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                NHAL---EKYKG 367
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       439 ANIICGDAKKKG 450
                                    WPI; 2001-592540/67
                                                                                                                                                                                                                                                                                                          474 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              10-MAR-2000
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    WO9955871-A1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            23-APR-1998;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     20-APR-1999;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             04-NOV-1999,
                                                                                                                                                                                                                                                                                                            Seguence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     AAY59353,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      BASB011
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   RESULT 11
AAY59353
                                                                                                                                                                                                                                                                                                                                                                                                                                8
                                                                                                                                                                                                                                                                                                                                                                                                                                                                         68
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        149
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 124
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          208
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  184
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        325
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 302
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                359
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Q,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       a
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     å
                                                                                                                                                                                                                                                                                                                                                                                                                                                                      g
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ò
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      8
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               δ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     g
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  à
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  g
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ò
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ద
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ŏ
```

```
5
                                                                                                                                                                                                                                                                                                                                                                                                      This sequence represents a BASB011 protein from Moraxella catarrhalis. The polypeptide is used to generate an immune response in an animal, particularly against a bacterial infection, e.g. a Moraxella catarrhalis infection. M. catarrhalis is present in 15% of childhood middle ear infections in the US. Molecules of the invention may also be used to prevent adhesion of bacteria to extracellular matrix proteins on inwounds, to block bacterial adhesion between extracellular matrix proteins and BASB011 proteins that mediate tissue damage, or to block the normal progression of pathogenesis in infections initiated other than by implanting of indwelling devices or by other
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         BASB011; immune response; bacterial infection; middle ear infection;
bacterial adhesion; extracellular matrix protein; tissue damage; therapy.
polypeptides from Moraxella catarrhalis used to treat the infection
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  131 LGSGVVVSSEGY1VTNAHVINGADEITVAL-NDGRKARATVIGSDADSDLAVIKVELDNL 189
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             PTIKFSDSNDISVGDLVFAIGNPFGVGESVTQGIVSALNKSGIGINSYENFIQTDASINP 130
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    191 GLQDLSGDLQNSYDNKEGAVVISVEKDSPAKKAGILVWDLITEVNGKKVKNTNELRNLIG 250
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           251 SMLPNQRVTLKV1.RDKKERAFTLTLAERKNPNKKETIS--AQNGAQGQLNGLQVEDLTQE 308
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       GNSGGALIDSRGGLVGINTAIISKTGGNHGIGFAIPSNMVKDTVTQLIKTGKIERGYLGV 190
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  : :: | | :: :: | | :: : | | :: | | :: | | :: | | :: | | :: | | :: | | :: | | :: | | :: | | :: | | :: | | :: | | :: | | :: | | | :: | | | :: | | | :: | | | :: | | | :: | | | :: | | | :: | | | :: | | | :: | | | :: | | | :: | | | :: | | | :: | | | :: | | | :: | | | :: | | :: | | :: | | :: | | :: | | :: | | :: | | :: | | | :: | | :: | | :: | | :: | | :: | | :: | | :: | | :: | | :: | | :: | | :: | | :: | | :: | | :: | | :: | | :: | | :: | | :: | | :: | | :: | | :: | | :: | | :: | | :: | | :: | | :: | | :: | | :: | | :: | | :: | | :: | | :: | | :: | | :: | | :: | | :: | | :: | | :: | | :: | | :: | | :: | | :: | | :: | | :: | | :: | | :: | | :: | | :: | | :: | | :: | | :: | | :: | | :: | | :: | | :: | | :: | | :: | | :: | | :: | | :: | | :: | | :: | | :: | | :: | :: | | :: | :: | | :: | :: | | :: | :: | | :: | :: | | :: | :: | | :: | :: | | :: | :: | | :: | :: | | :: | :: | :: | | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: |
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 8;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Length 433;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Query Match 35.2%; Score 683; DB 21; Best Local Similarity 45.3%; Pred. No. 4.5e-47; Matches 136; Conservative 73; Mismatches 83;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Ş
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            AAY59354 standard; Protein; 433
                                                                                                                                                                                                                                                              Claim 3; Fig 3; 168pp; English
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                BASB011 protein sequence #2.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           9910-EP02764
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               (first entry)
```

```
The polypeptide is used to generate an immune response in an animal, particularly against a bacterial infection, e.g. a Moraxella catarrhalis infection. M. catarrhalis is present in 15% of childhood middle ear infections in the US. Molecules of the invention may also be used to prevent adhesion of bacteria to extracellular matrix proteins on inducibiling devices or in wounds, to block bacterial adhesion between extracellular matrix proteins and BASBO11 proteins that mediate tissue damage, or to block the normal progression of pathogenesis in infections initiated other than by implanting of indwelling devices or by other
                                                                                                                                                                                              polypeptides from Moraxella catarrhalis used to treat the infection
                                                                                                                                                                                                                                                                                                         This sequence represents a BASB011 protein from Moraxella catarrhalis.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        249 GNSGGALVDANGALIGINTAIYSRSGGSMGIGFAIPNQIVQQVMTSLITTGKVSRGWMGI 308
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               GNSGGALIDSRGGLVGINTAIISKTGGNHGIGFAIPSNMVKDTVTQLIKTGKIERGYLGV 190
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 71 PTIKFSDSNDISVGDLVFAIGNPFGVGESVTQGIVSALNKSGIGINSYENFIQTDASINP 130
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          309 EMVRMTDDPTN-IESRSNVIIRRVWQNSPAEHAGLKSGDKIVRIDGVHITSINELVGVVA 367
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  11 LGSGVIISKDGYIVTNNHVIDGADKIKVTIPGSNKEYSATLVGTDSESDLAVIRITKDNL 70
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     GLQDLSGDLQNSYDNKEGAVVISVEKDSPAKKAGILVWDLITEVNGKKVKNTNELRNLIG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       SMLPNORVTLKVIRDKKERAFTLTLAERKNPNKKETIS--AQNGAQGQLNGLQVEDLTQE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  35.2%; Score 683; DB 21; Length 433; 45.3%; Pred. No. 4.5e-47; ive 73; Mismatches 83; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Human pathogen; virulence polypeptide; virulence factor; pathogenic infection; Pseudomonas aeruginosa infection.
                                        (SMIK ) SMITHKLINE BEECHAM BIOLOGICALS.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Protein encoded by the PA14 degP gene.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ¥.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           AAY29294 standard; Protein; 460
                                                                                                                                                                                                                                                                Claim 3; Fig 3; 108pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     98WO-US25247.
  98GB-0008720
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Matches 136; Conservative
                                                                                                                              WPI; 2000-062033/05
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Query Match
Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           433 AA;
                                                                                                                                                     N-PSDB; AAZ48702
                                                                                                                                                                                                                     this bacteria
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               W09927129-A1.
23-APR-1998;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     25-NOV-1998;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 25-OCT-1999
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          03-JUN-1999
                                                                                        Ruelle J;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               131
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   191
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  368
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        AAY 29294
  g
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      g
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            g
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                g
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ò
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ò
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ò
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ò
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 3
                                                                                                                                                                                                                                                                                                    The polypeptide is used to generate an immune response in an animal, infection. A gainst a bacterial infection, e.g. a Moraxella catarrhalis infection. M. catarrhalis is present in 18% of childhood middle ear infections in the US. Molecules of the invention may also be used to prevent adhesion of bacteria to extracellular matrix proteins on indwelling devices or in wounds, to block bacterial adhesion between extracellular matrix proteins and BASBOII proteins that mediate tissue damage, or to block the normal progression of pathogenesis in infections initiated other than by implanting of indwelling devices or by other
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            BASB011; immune response; bacterial infection; middle ear infection;
bacterial adhesion; extracellular matrix protein; tissue damage; therapy.
                                                                                                                                                          , polypeptides from Moraxella catarrhalis used to treat the infection this bacteria -
                                                                                                                                                                                                                                                                                  This sequence represents a BASB011 protein from Moraxella catarrhalis.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          71 PTIKFSDSNDISVGDLVFAIGNPFGVGESVTQGIVSALNKSGIGINSYENFIQTDASINP 130
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       131 GNSGGALIDSRGGLVGINTAIISKTGGNHGIGFAIPSNMVKDTVTQLIKTGKIERGYLGV 190
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               249 GNSGGALVDANGALIGINTAIYSRSGGSMGIGFAIPNQIVQQVWISLITTGKVSRGWMGI 308
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          191 GLQDLSGDLQNSYDNKEGAVVISVEKDSPAKKAGILVWDLITEVNGKKVKNTNELRNLIG 250
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        251 SMLPNQRVTLKVIRDKKERAFTLTLAERKNPNKKETIS--AQNGAQGQLNGLQVEDLTQE 308
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 11 LGSGVIISKDGYIVTNNHVIDGADKIKVTIPGSNKEYSATLVGTDSESDLAVIRITKDNL 70
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          8;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Length 433;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          83; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         35.2%; Score 683; DB 21;
45.3%; Pred. No. 4.5e-47;
11ve 73; Mismatches 83;
                    (SMIK ) SMITHKLINE BEECHAM BIOLOGICALS.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ¥.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  AAY59355 standard; Protein; 433
                                                                                                                                                                                                                                       Claim 3; Fig 3; 108pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               99WO-EP02764.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   BASB011 protein sequence #3.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Matches 136; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Moraxella catarrhalis.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         surgical techniques.
                                                                                                      WPI; 2000-062033/05
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  433 AA;
                                                                                                                              N-PSDB; AAZ48701
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            20-APR-1999;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        10-MAR-2000
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         WO9955871-A1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 04-NOV-1999
                                                               Ruelle J;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               AAY59355;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Query Match
```

g

à

ò

g

ò q

ò

3

SULT 13 AY59355

8 ŏ

5

Gaps

```
qq
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             qq
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ò
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 g
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          g
                                                                                                                                                                                                                                                                                                                                                                                                                                                                              à
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  g
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       δ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ò
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    g
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ò
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ά
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       g
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ò
                                                                                                                                                                                                                                                                                                                                         ж
;
                                                                                                                                                       sequence. P. aeruginosa is an opportunistic human pathogen present in soll water and plants. The specification describes virulence polypeptides and nucleic acid sequence enopound which is capable of decreasing the expression of a pathogenic virulence factor. Compounds that inhibit the expression or activity of virulence factor polypeptides can be used to treat pathogenic infections, especially where the infection is a P. aeruginosa infection. especially where the infection note: the sequences given in the specification were poorly legible, and in some instances assumptions were made as to the identity of the residue; it is therefore possible that the sequence given below is
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  298
                                                                                                                                                                                                                                                                                                                                                                        RITKDNLPTIKFSDSNDISVGDLVFAIGNPFGVGESVTQGIVSALNKSGIGINSYENFIQ 123
                                                                                                                                                                                                                                                                                                                                                                                                                                              TDASINPGNSGGALIDSRGGLVGINTAIISKTGGNHGIGFAIPSNMVKDTVTQLIKTGKI 183
                                                                                                                                                                                                                                                                                                                                                                                                                                                                    267
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    384
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ERGYLGVGLQDLSGDLQNSY - - DNKEGAVVISVEKDSPAKKAGILVWDLITEVNGKKVKN 241
                                                                                                                                                                                                                                                                                                                                          Gaps
                                                                                                                                                                                                                                                                                                                                                           4 KERMERALGSGVIISKDGYIVTNNHVIDGADKIKVTIPGSNKEYSATLVGTDSESDLAVI 63
                                                                                                                                                present sequence represents a Pseudomonas aeruginosa polypeptide
                                                                                                                                                                                                                                                                                                                                                                                                                                                         TNELRNLIGSMLPNQRVTLKVIRDKKERAFTLTLAERKNPNKKETISAQNGAQGQLN---
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           --GLQVEDLTQETKRSMRLSDDVQGVLVSQVNENSPAEQAGFRQGNIITKIEEVEVKSV-
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             SADLPHLYGMMKPGDKINLDVIRMGQRK--SLSMAVGNLPDDDEEI-ASMGAPGAERSSM
                                                    ŝ
                                                                                                                                                                                                                                                                                                                     Length 460;
                                                   Mahajan-Miklos
                                                                                                     Virulence factors useful in developing disease treatments
                                                                                                                                                                                                                                                                                                                  35.2%; Score 681.5; DB 20; Length 41.3%; Pred. No. 6.5e-47; ive 72; Mismatches 132; Indels
                                                   Goodman HM,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            AAR92690 standard; Protein; 463 AA.
                                                                                                                           Disclosure; Fig 28; 228pp; English
                                                   ij.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        IFADVAKALPKMRSVSMRVL 460
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   --ADFNHALEKYKGKPKRFL 373
                                                  Cao H, Drenkard
Tan M, Tsongalis
         97US-0066517
                              (GEHO ) GEN HOSPITAL CORP.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       (first entry)
                                                                                                                                                                                                                                                                                                                              Best Local Similarity 41.3
Matches 157; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           H. influenzae SB33 Hin47
                                                                                                                                                                                                                                                                          not entirely correct.
                                                                                 WPI; 1999-357851/30.
                                                                                                                                                                                                                                                                                                               Query Match
Best Local Similarity
                                                                                                                                                                                                                                                                                              460 AA;
         25-NOV-1997;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      03-JUN-1996
                                                  Ġ,
                                                             Rahme LG,
                                                                                                                                                                                                                                                                                                Seguence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 AAR92690;
                                                  Ausubel
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        441
                                                                                                                                                                                                                                                                                                                                                                                                     . 49
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 242
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     328
                                                                                                                                                                                                                                                                                                                                                                                                                        149
                                                                                                                                                                                                                                                                                                                                                                                                                                              124
                                                                                                                                                                                                                                                                                                                                                                                                                                                                  208
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       184
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            268
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   AAR92690
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ò
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           g
g
                                                                                                                                                                                                                                                                                                                                                                                                     ŏ
                                                                                                                                                                                                                                                                                                                                                                                                                        g
                                                                                                                                                                                                                                                                                                                                                                                                                                            δ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                à
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   g
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         á
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            g
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   à
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      셤
```

```
Outer membrane protein Hin47 (AAR92690) of H. influenzae SB33 is reported to be an Adhesin, and is conserved among strains of H. influenzae. For Hin47 to be used in vaccines, its protease activity must be decreased to prevent degradation of other antigens. This was performed by site-directed mutagenesis of the hin47 gene (AAT10423). Hin47 analogues in which e.g. Ser197 was replaced by Ala, Cys or Thr, His91 by Ala, Lys or Arg, or Asp121 by Ala were produced by transformed host cells. The analogues had less than 10% of the protease activity of native Hin47. They can also be used to raise antibodies and as carriers in prodn. of conjugate vaccines.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                RITK-DNLPTIKFSDSNDISVGDLVFAIGNPFGVGESVTQGIVSALNKS-GIGINSYENF 121
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  182 KIERGYLGVGLQFLSGDLQNSYD--NKEGAVVISVEKDSPAKKAGILVWDLITEVNGKKV 239
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               NGLQVEDLTQETERSMRLSDDVQGVLVSQVNENSPAEQAGFRQGNIITKIEEVEVKSVAD 357
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    H.influenzae Hin47 protein analogue with decreased protease activity - and nucleic acid encoding it, useful in vaccines and as diagnostic
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ERMERALGSGVII-SKDGYIVTNNHVIDGADKIKVTIPGSNKEYSATLVGTDSESDLAVI 63
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             240 KNTNELRNLIGSMLPNQRVTLKVIRDKKERAFTLTLA--ERKNPNKKETISAQNGAQGQL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                122 IQTDASINPGNSGGALIDSRGGLVGINTAIISKTGGNHGIGFAIPSNMVKDTVTQLIKTG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    24;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Length 463;
protease; mutagenesis; vaccine; diagnosis;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 34.4%; Score 666; DB 17; Length 4, 41.0%; Pred. No. 1.2e-45; ive 75; Mismatches 117; Indels
                                                                                                                                                                                                                                                                                                                                                                                                               Υ;
                                                                                                                                                                                                                                                                                                                                                                                                               Yang
                      meningitis; epiglotitis, pneumonia; otitis media
                                                                                                                                                                                                                                                                                                                                                                                                               RP,
                                                                                                                                                                                                                                                                                                                                                                                                                  Oomen
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Example 2; Fig 2A-2H; 75pp; English.
                                                                      Haemophilus influenzae strain SB33
                                                                                                                                                                                                                                                                                                                                                                                                               SM,
                                                                                                                                                                                                                                                                                                                                                                                                               Chong P, Klein MH. Loosmore
                                                                                                                                                                                                                                                                                      94US-0278091.
                                                                                                                                                                                                                    95WO-CA00434
                                                                                                                                                                                                                                                                    95US-0487167
                                                                                                                                                                                                                                                                                                                                                                  (CONN-) CONNAUGHT LAB LID.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Query Match
Best Local Similarity 41.0°
Matches 150; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                          WPI; 1996-117051/12.
N-PSDB; AAT10423.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         463 AA;
  Hin47; adhesin;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  363
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                441
                                                                                                                                                                                                                                                                                      21-JUL-1994;
26-AUG-1994;
                                                                                                                    WO9603506-A2
                                                                                                                                                                                                                    21-JUL-1995;
                                                                                                                                                                                                                                                                  07-JUN-1995;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                FNHALE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             LNKVLE
                                                                                                                                                                    08-FEB-1996
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Seguence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Ŋ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 64
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               298
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                358
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               385
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                436
```

.; 8

Search completed: November 18, 2002, 11:28:36 Job time : 41 secs

```
This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
                                 mus musculu
                                             salmonella
campylobact
                                                                             staphylococ
                                                                                                             campylobact
                                                                                                                            p genome po
escherichia
                                                                                                                                                          p genome po
 saccharomyc
                  aguifex aeo
                                                                                               mycoplasma
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    STRAIN=D/UW-3/Cx;
MEDILINE-99000809; PubMed-9784136;
Stephens R.S., Kalman S., Lammel C.J., Fan J., Marathe R., Aravind L.,
Aitchell W.P., Olinger L., Tatusov R.L., Zhao Q., Koonin E.V.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Genome sequence of an obligate intracellular pathogen of humans:
Chlamydia trachomatis.";
Science 282:754-754(1998).
Science 282:776-759(1998).
-!- SIMILARITY: BELONGS TO PEPTIDASE FAMILY S2C.
-!- SIMILARITY: BELONGS TO PEPTIDASE FAMILY S2C.
-!- CUUTION: REP.1 SEQUENCE NAS INCORRECT: DUE TO SEQUENCING ERRORS
-!- CAUTION: REP.1 SEQUENCE THER PUTATIVE 59 kDa IMMUNOGENIC PROTEIN
ON THE COMPLEMENTARY STRAND TO THAT OF WHAT SEEMS TO BE THE REAL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Kahane S., Weinstein Y., Sarov I.; "Cloning, characterization and sequence of a novel 59-kDa protein of Chlamydia trachomatis.";
                                                                                                                                                                                                                                                                                                  DEGP_CHLTR STANDARD; PRT; 497 AA.
P18584; 084830;
01-NOV-1990 (Rel. 16, Created)
01-NOV-2000 (Rel. 39, Last sequence update)
15-JUN-2002 (Rel. 41, Last annotation update)
Probable serine protesse do like precursor (EC 3.4.21.-) (59 kDa immunogenic protein) (SK59).
               067776
035435
P22927
P22927
Q53654
Q53654
Q01681
Q01681
P33666
P17767
                                                                                                                                                                                                                                                                                                                                                                                                                                       Chlamydia trachometis.
Bacteria; Chlamydiales; Chlamydiaceae; Chlamydia.
NCBI_TaxID=813;
                                                                                                                                                                                                                            ALIGNMENTS
               YJ64_AQUAE
PYRD_MOUSE
BIGA_SALTY
FLB2_CAMJE
CNA_STAAU
RPOB_MYCGA
                                                                                                           FLA2_CAMJE
POLG_PPVEA
YDBA_ECOLI
POLG_PPVRA
POLG_PPVD
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           InterPro; IPR000126; Ser_proteas_V8.
InterPro; IPR001254; Ser_protease_Try.
Pfam; PF00089; rrypsin; 1.
Pfam; PF00595; PDZ; 2.
PRINTS; PR00834; FROTEASES2C.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    STRAIN=Serovar L2;
MEDLINE=90337348; PubMed=2379836;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             InterPro; IPR001940; Protease2C
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            EMBL; AE001355; AAC68420.1; -
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           EMBL; M31119; AAAZ3116.1; -. PHCI-2DPAGE; P18584; -. InterPro; IPR001478; PDZ.
997
429
395
1953
11183
1390
1518
2003
3140
                                                                                                                                                                                                                                                                                                                                                                                                                           DEGP OR HTRA OR CT'823
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   3ene 90:61-67(1990).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   PROTEIN.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Davis R.W.;
136.5
126
125
123
122
122
122
112
117.5
1117.5
1116.5
                                                                                                                                                                                                                                                                           RESULT 1
 P18584 chlamydia to 1990
09p197 chlamydia m
P09376 escherichia o 1989
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                505
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     brucella abe
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   buchnera ap
escherichia
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              09z6t0 chlamydia p
P26982 salmonella e
Q44597 brucella ab
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  244947≈haemophilus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   buchnera ap
rickettsia
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    rhizobium m
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   escherichia
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  bacillus su
bacillus su
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  arabidopsis
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 arabidopsis
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  lactococcus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            mus musculu
rhizobium s
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   bartonella (
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  bacillus su
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 homo sapien
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 mus musculu
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 mus musculu
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              homo sapien
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               arabidopsis
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              staphylococ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               lactobacill
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               homo sapien
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 homo sapien
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    rickettsia
                                                                                                                              (without alignments)
1146.524 Million cell updates/sec
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Description
                                                                                                                                                                                          1938
1 MIPKERMERALGSGVIISKD.....KPKRFLVLDLNQGYRIILVK
                                                                                                             November 18, 2002, 11:20:03; Search time 14 Seconds
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                P45129
P57322
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                092ja1
085291
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                P39099
005942
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Q52894
P54925
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               034358
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             091u10
P39668
0924h7
091a06
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Q92743
Q9r118
P83110
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            09jiy5
P83105
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           09d236
P55377
P09331
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 P31137
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            043464
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               09sel7
                GenCore version 5.1.3
Copyright (c) 1993 - 2002 Compugen Ltd
                                                                                                                                                                                                                                                                                                                        Total number of hits satisfying chosen parameters:
                                                                                                                                                                                                                                                                                          112892 seqs, 41476328 residues
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       SUMMARIES
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           HRA2_MOUSE
HRA4_HUMAN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 DEGP_BUCAI
DEGP_RICCN
DEGP_BUCAP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             DEG8_ARATH
YYXA_BACSU
HTRA_LACHE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              HTRA_LACLA
HRA1_HUMAN
HRA1_MOUSE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 DEGP_CHLPN
DEGP_SALTY
DEGP_BRUAB
HTOA_HAEIN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 DEGP_RICPR
DEGP_RHIME
DEGP_BARHE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   DEGS_ECOLI
YVTA_BACSU
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              HTRA_BACSU
DEG1_ARATH
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             HHOA_ARATH
HRA3_MOUSE
Y4BJ_RHISN
ETA_STAAU
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     DEGP_CHLMU
DEGP_ECOLI
                                                                                                                                                                                                                                                                                                                                                                                                                          Maximum Match 100%
Listing first 45 summaries
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  DEGS_HAEIN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               HRA3_HUMAN
                                                                              OM protein - protein search, using sw model
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    DEGP_CHLTR
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  DEGO_ECOLI
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              HRA2_HUMAN
                                                                                                                                                                                                                                           BLOSUM62
Gapop 10.0 , Gapext 0.5
                                                                                                                                                                              US-09-895-913A-120
                                                                                                                                                                                                                                                                                                                                                          Minimum DB seq length: 0
Maximum DB seq length: 2000000000
                                                                                                                                                                                                                                                                                                                                                                                                          Post-processing: Minimum Match 0%
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      DB
                                                                                                                                                                                                                                                                                                                                                                                                                                                                         SwissProt_40:*
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Length
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Query
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    749.5
746.5
7722.5
714.5
714.5
679.5
663.5
663.5
657.5
618.5
618.5
618.5
618.5
618.5
618.5
618.5
618.5
618.5
618.5
618.5
618.5
618.5
618.5
618.5
618.5
618.5
618.5
618.5
618.5
618.5
618.5
618.5
618.5
618.5
618.5
618.5
618.5
618.5
618.5
618.5
618.5
618.5
618.5
618.5
618.5
618.5
618.5
618.5
618.5
618.5
618.5
618.5
618.5
618.5
618.5
618.5
618.5
618.5
618.5
618.5
618.5
618.5
618.5
618.5
618.5
618.5
618.5
618.5
618.5
618.5
618.5
618.5
618.5
618.5
618.5
618.5
618.5
618.5
618.5
618.5
618.5
618.5
618.5
618.5
618.5
618.5
618.5
618.5
618.5
618.5
618.5
618.5
618.5
618.5
618.5
618.5
618.5
618.5
618.5
618.5
618.5
618.5
618.5
618.5
618.5
618.5
618.5
618.5
618.5
618.5
618.5
618.5
618.5
618.5
618.5
618.5
618.5
618.5
618.5
618.5
618.5
618.5
618.5
618.5
618.5
618.5
618.5
618.5
618.5
618.5
618.5
618.5
618.5
618.5
618.5
618.5
618.5
618.5
618.5
618.5
618.5
618.5
618.5
618.5
618.5
618.5
618.5
618.5
618.5
618.5
618.5
618.5
618.5
618.5
618.5
618.5
618.5
618.5
618.5
618.5
618.5
618.5
618.5
618.5
618.5
618.5
618.5
618.5
618.5
618.5
618.5
618.5
618.5
618.5
618.5
618.5
618.5
618.5
618.5
618.5
618.5
618.5
618.5
618.5
618.5
618.5
618.5
618.5
618.5
618.5
618.5
618.5
618.5
618.5
618.5
618.5
618.5
618.5
618.5
618.5
618.5
618.5
618.5
618.5
618.5
618.5
618.5
618.5
618.5
618.5
618.5
618.5
618.5
618.5
618.5
618.5
618.5
618.5
618.5
618.5
618.5
618.5
618.5
618.5
618.5
618.5
618.5
618.5
618.5
618.5
618.5
618.5
618.5
618.5
618.5
618.5
618.5
618.5
618.5
618.5
618.5
618.5
618.5
618.5
618.5
618.5
618.5
618.5
618.5
618.5
618.5
618.5
618.5
618.5
618.5
618.5
618.5
618.5
618.5
618.5
618.5
618.5
618.5
618.5
618.5
618.5
618.5
618.5
618.5
618.5
618.5
618.5
618.5
618.5
618.5
618.5
618.5
618.5
618.5
618.5
618.5
618.5
618.5
618.5
618.5
618.5
618.5
618.5
618.5
618.5
618.5
618.5
618.5
618.5
618.5
618.5
618.5
618.5
618.5
618.5
618.5
618.5
618.5
618.5
618.5
618.5
618.5
618.5
618.5
618.5
618.5
618.5
618.5
618.5
618.5
618.5
618.5
618.5
618.5
618.5
618.5
618.5
618.5
618.5
618.5
618.5
618.5
618.5
618.5
618.5
618.5
618.5
618.5
618.5
618.5
618.5
618.5
618.5
618.5
618.5
618.5
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               474.5
451.5
439
414.5
414.5
380.5
380.5
348.5
348.5
340.5
334.5
3357.5
3348.5
3348.5
3348.5
3348.5
3348.5
346.5
346.5
346.5
                                                                                                                                                                                                                                           coring table:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Score
                                                                                                                                                                                            Perfect score:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Database :
                                                                                                                                                                                                             Sequence:
                                                                                                                                                                                                                                                                                            Searched:
                                                                                                              Run on:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Result
                                                                                                                                                                              Title:
```

```
DEGP_ECOLI

ID DEGP_ECOLI STANDARD; PRT; 474 AA.

R P09376; P15724;

DT 01-MAR-1989 (Rel. 10, Created)

DT 15-JUN-2002 (Rel. 41, Last sequence update)
  -!- SIMILARITY: CONTAINS 2 PDZ/DHR DOMAINS.
                                                                                                                                            InterPro; IPR001478; PD2.
InterPro; IPR001478; PD2.
InterPro; IPR00126; Ser_proteas_V8.
InterPro; IPR00125; Ser_protease_Try.
Pfam; PF00089; trypsin; I.
Pfam; PF00089; trypsin; I.
PRINTS; PR00834; PROTEASES.C.
PRINTS; PR00839; V8PROTEASE.
SWARR; SM00228; PDZ; 2.
                                                                                                                                                                                                                                                                                                  CATALYTIC.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             360 HALEKYKGKPKRFLVLDLNQG--YRIILVK 387
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Repeat;
                                                                                                                 EMBL; AE002288; AAF39082.1; -.
                                                                                                                                                                                                                                                                                                                                                                    53294 MW;
                                                                                                                                                                                                                                                  PROSITE; PS50106; PDZ; 2.
Hydrolase; Serine protease;
                                                                                                                                                                                                                                                                                                                                                                                        Query Match
Best Local Similarity 41.3%;
Matches 161; Conservative
                                                                                                                                                                                                                                                                                                                                            173
247
497 AA;
                                                                                                                              MEROPS; S01.273;
                                                                                                                                     TIGR; TC0210;
                                                                                                                                                                                                                                                                                                                                            ACT_SITE
ACT_SITE
SEQUENCE
                                                                                                                                                                                                                                                                                                                                    ACT_SITE
                                                                                                                                                                                                                                                                            SIGNAL
                                                                                                                                                                                                                                                                                                  DOMAIN
                                                                                                                                                                                                                                                                                                            DOMAIN
                                                                                                                                                                                                                                                                                                                       DOMAIN
                                                                                                                                                                                                                                                                                       CHAIN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             123
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 237
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              297
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     241
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 300
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     RESULT
   ð
                                                                                                                                                                                                                                                                                                                                                                                                                                                           g
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ò
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     8
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ò
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 g
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       à
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              g
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ŏ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        g
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ð
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     셤
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 g
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             à
                                                                                                                                                                                               7;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     [1]
SEQUENCE FROM N.A.
STRAIN-MOPD / Nigg;
MEDLINE-20150255; PubMed-10684935;
Read T.D., Brunham R.C., Shen C., Gill S.R., Heidelberg J.F.,
White O., Hickey E.K., Peterson J., Utterback T., Berry K., Bass S.,
Linher K., Welldman J., Khouri H., Craven B., Bowman C., Dodson R.,
Gwinn M., Nelson W., DeBoy R., Kolonay J., McClarty G., Salzberg S.L.,
Eisen J., Fraser C.M.;
                                                                                                                                                                                                                                                                                                                                                                                                     299
                                                                                                                                                                                                                             63 IRITKDNLPTIKFSDSNDISVGDLVFAIGNPFGVGESVTQGIVSALNKSGIGINSYENFI 122
                                                                                                                                                                                                                                                                          183 IERGYLGVGLQDLSGDLQNSY--DNKEGAVVISVEKDSPAKKAGILVWDLITEVNGKKVK 240
                                                                                                                                                                                                                                                                                                                                                                                                                          407
                                                                                                                                                                                                                                                                                                                                                                                                                                             300 LQVEDLTQETKRSMRLSDDVQGVLVSQVNENSPAEQAGFRQGNIITKIEEVEVKSVADFN 359
                                                                                                                                                                                                                                                                                                                                                                                                                                                                      467
                                                                                                                                                                                                                                                                                                           QTDASINPGNSGGALIDSRGGLVGINTAIISKTGGNHGIGFAIPSNMVKDTVTQLIKTGK 182
                                                                                                                                                                                               Gaps
                                                                                                                                                                                                                    62
                                                                                                                                                                                                                 3 PKERMERALGSGVIISKDGYIVTNNHVIDGADKIKVTIPGSNKEYSATLVGTDSESDLAV
                                                                                                                                                                                                                                                                                                                                                                                                 241 NTNELRNLIGSMLPNQRVTLKVIRDKKERAFTLTLAERKNPNKKETISAQNGAQG-QLNG
                                                                                                                                                                                                                                                                                                                                                                                                                                                          19;
                                                                   SERINE PROTEASE DO-LIKE.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     "Genome sequences of Chlamydia trachomatis MoPn and Chlamydia pneumoniae AR39.";
Nucleic Acids Res. 28:1397-1406(2000).
-I- SIMILARITY: BELONGS TO PEPTIDASE FAMILY S2C.
                                                                                                                                                                        DB 1; Length 497;
                                                                                                           CHARGE RELAY SYSTEM (POTENTIAL).
CHARGE RELAY SYSTEM (POTENTIAL).
CHARGE RELAY SYSTEM (POTENTIAL).
86A5E31BB84A38BA CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         16-OCT-2001 (Rel. 40, Created)
16-OCT-2001 (Rel. 40, Last sequence update)
15-JUN-2002 (Rel. 41, Last annotation update)
Probable serine protease do-like precursor (EC 3.4.21.-).
DEGP OR HTRA OR TC0210.
                                                                                                                                                                                             126; Indels
                                  Repeat; Signal; Antigen;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Chlamydia muridarum.
Bacteria; Chlamydiales; Chlamydiaceae; Chlamydia.
                                                                                                                                                                      ; Score 749.5; DB 1
; Pred. No. 4.6e-37;
84; Mismatches 126
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ¥.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       497
                                                                   PROBABLE SE
                                                        POTENTIAL.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        360 HALEKYKGKPKRFLVLDLNQG--YRIILVK 387
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        |::| | |::| 494
                                                                                                                                                 53244 MW;
                                                                                                                                                                       38.7%;
41.3%;
                      PROSITE; PS50106; PDZ; 2.
Hydrolase; Serine protease;
PR00839; V8PROTEASE. SM00228; PDZ; 2.
                                                                                                                                                                                             Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       STANDARD;
                                                        16
497
289
381
485
                                                                           128
290
394
143
173
247
497 AA;
                                                                                                                                                                                  Local Similarity
                                           Complete proteome
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            NCBI_TaxID=83560;
                                                                                                                                                                                             Matches 161:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      DEGP_CHI_MU
                                                                                                              ACT_SITE
ACT_SITE
ACT_SITE
SEQUENCE
                                                                                                                                                                       Match
PRINTS;
SMART; S
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               09PL97;
                                                                  CHAIN
DOMAIN
DOMAIN
DOMAIN
                                                       SIGNAL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 RESULT 2
DEGP_CHLMU
                                                                                                                                                                                                                                                                                                          123
                                                                                                                                                                                  Best
 셤
                                                                                                                                                                                                                                                                                                                                g
                                                                                                                                                                                                                                                                                                                                                                                                 ò
                                                                                                                                                                                                                                                                                                                                                                                                                      셤
                                                                                                                                                                                                                                                                                                                                                                                                                                                                 셤
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          à
                                                                                                                                                                                                                   à
                                                                                                                                                                                                                                                              à
                                                                                                                                                                                                                                                                                                          ò
                                                                                                                                                                                                                                                                                                                                                       õ
                                                                                                                                                                                                                                                                                                                                                                            셤
                                                                                                                                                                                                                                                                                                                                                                                                                                              à
```

```
This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ζ,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          236
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        183 IERGYLGVGLQDLSGDLQNSY--DNKEGAVVISVEKDSPAKKAGILVWDLITEVNGKKVK 240
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           63 IRITKDNLPTIKFSDSNDISVGDLVFAIGNPFGVGESVTQGIVSALNKSGIGINSYENFI 122
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        QTDASINPGNSGGALIDSRGGLVGINTAIISKTGGNHGIGFAIPSNMVKDTVTQLIKTGK 182
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      296
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          407
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       408 VRVQNLTPEICKKLGLASDTRGIFVVSVEAGSPAASAGVVPGOLILAVNRQRVSSVEELN 467
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    3 PKERMERALGSGVIISKDGYIVTNNHVIDGADKIKVTIPGSNKEYSATLVGTDSESDLAV 62
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           177 IKIQAKNLPFLTFGNSDQLQIGDWSIAIGNPFGLQATVTVGVISAKGRNQLHIVDFEDFI
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         NTNELRNLIGSMLPNQRVTLKVIRDKKERAFTLTLAERKNPNKKETISAQNGAQG-QLNG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          357 SLSALRNAISLAMPGTRVVLKVVREGKFIEIPVTVTQ-----IPAEDGVSALQKMG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            LQVEDLTQETKRSMRLSDDVQGVLVSQVNENSPAEQAGFRQGNIITKIEEVEVKSVADFN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    POTENTIAL.
PROBABLE SERINE PROTEASE DO-LIKE.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Signal; Complete proteome.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Length 497;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             CHARGE RELAY SYSTEM (POTENTIAL)
CHARGE RELAY SYSTEM (POTENTIAL)
CHARGE RELAY SYSTEM (POTENTIAL)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   38.5%; Score 746.5; DB 1;
41.3%; Pred. No. 6.9e-37;
ive 84; Mismatches 126;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     B765F350ACC66BBF
```

m

```
STRAIN-0157:H7 / RIMD 0509952;
MEDLINE-21156231; PubMed=11258796;
Hayashi T., Makino K., Ohnishi M., Kurokawa K., Ishii K., Yokoyama K., Han C.-G., Ohtsubo E., Nakayama K., Murata T., Tanaka M., Tobe T., Iida T., Takami H., Honda T., Sasakawa C., Ogasawara N., Yasunaga T., Kuhara S., Shiba T., Hattori M., Shinagawa H.;
"Complete genomic compence of enterohemorrhagic Escherichia coli Ol57:H7 and genomic comparison with a laboratory strain K-12.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             SEQUENCE FROM N.A.
STRAIN=KIZ / MG1657;
STRAIN=KIZ / MG167;
PubMed=9278503;
Blattiner F.R., Plunkett G. III, Bloch C.A., Perna N.T., Burland V.,
Riley M., Collado-Vides J., Glasner J.D., Rode C.K., Mayhew G.F.,
Gregor J., Davis N.W., Kirkpatrick H.A., Goeden M.A., Rose D.J.,
Mau B., Shao Y.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               STRAIN-0157:H7 / EDL933 / ATCC 700927;
MEDLINE-21074935; PubMed=11206551;
MEDLINE-21074935; PubMed=11206551;
MEDLINE-21074935; PubMed=11206551;
Rose D.J., Maybew G.F., Evans P.S., Gregor J., Kirkpatrick H.A., Posfai G., Hackett J., Klink S., Boutin A., Shao Y., Miller L., Grotbeck E.J., Davis N.W., Lim A., Dimalanta E.T., Potamousis K., Apodaca J., Anantharaman T.S., Lin J., Yen G., Schwartz D.C., Welch R.A., Blattner F.R.;
"Genome sequence of enterohaemorrhagic Escherichia coli 0157:H7.";
                                                                                                                                                                                                                                                                                                                                                                                                                 Fujita N., Mori H., Yura T., Ishihama A.; Systematic sequenching of the Escherichia coli genome: analysis of the Scherichia coli genome: analysis of the 24-4.1 min (110,917-193.643 bp) region."; Nucleic Acids Res. 22:1637-1639(1994).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    .
Ш
                                                                                                                                                                                                                                   Lipinska B., Sharma S., Georgopoulos C.; "Sequence analysis and regulation of the htrA gene of Escherichia
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         SEQUENCE FROM N.A.
Schramm S., Duncan M., Allen E., Araujo R., Aparicio A., Chung E.
Davis K., Federspiel N., Hyman R., Kalman S., Komp C., Kurdi O.,
Lashkari D., Lew H., Lin D., Namath A., Oefner P., Roberts D.,
                                                          Escherichia coli, and
Escherichia coli 0157:H7..
Bacteria; Proteobacteria; gamma subdivision; Enterobacteriaceae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Quirk S., Bhatnagar S.K., Bessman M.J.; Primary structure of the deoxyguanosine triphosphate triphosphohydrolase-encoding gene (dgt) of Escherichia coli."; Gene 89:13-18(1990).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       "The complete genome sequence of Escherichia coli K-12."; Science 277:1453-1474(1997).
                                                                                                                                                                                                                                                                           coli: a sigma 32-independent mechanism of heat-inducible
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Submitted (SEP-1996) to the EMBL/GenBank/DDBJ databases.
15-JUN-2002 (Rel. 41, Last annotation update)
Protease do precursor (EC 3.4.21.-).
DEGP OR HTRA OR PTD OR B0161 OR 20173 OR ECS0165.
                                                                                                                                                                                                                                                                                              transcription.";
Nucleic Acids Res. 16:10053-10067(1988).
                                                                                                                                                                                                                                                                                                                                    [2]
SEQUENCE FROM N.A.
STRAIN-KI2 / W3110,
MEDLINE-94261430, PubMed-8202364;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              MEDLINE=90323597; PubMed=2165018;
                                                                                                                                                                                                                MEDLINE-89057448; PubMed-3057437;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          SEQUENCE OF 1-50 FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Nature 409:529-533(2001).
                                                                                                                                     NCBI_TaxID=562, 83334;
                                                                                                                                                                            SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    SEQUENCE FROM N.A.
                                                                                                                     Escherichia
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Davis R.W.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            STRAIN-K12
```

```
This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to licenseélsb-sib.ch).
                                                                                                                                                                                                                                                DEDITITY OF HTRA AND PROTEASE DO.

MEDLINE-91222240; PUDMEd-2025286;

Seol J.H., Woo S.K., Jung E.M., Yoo S.J., Lee C.S., Kim K.J.,

Seol J.H., Woo S.K., Jung E.M., Yoo S.J., Lee C.S., Kim K.J.,

Tanaka K., Ichihaka A., Ha D.B., Chung C.H.;

Throtease Do is essential for survival of Escherichia coll at high

temperatures: its identity with the htra gene product.";

Blochem. Blophys. Res. Commun. 176:730-736(1991).

-I FUNCTION: SERINE PROTEASE THAT IS REQUIRED AT HIGH TEMPERATURE.

INVOLVED IN THE DEGRADATION OF DAMAGED PROTEINS: IT CAN DEGRADES

COLLICAR ALCATION: PRAY SHOCK.

-I SUBUNIT: MULTIMERIC.

-I SUBUNIT: MULTIMERIC.

-I SUBULIARIZES AND GLOBIN. SHARED SPECIFICITY WITH DEGQ.

-I INDUCTION: BY HEAT SHOCK.

-I INDUCTION: BY HEAT SHOCK.

-I MISCELLANEOUS: HTRA IS INDISPENSABLE FOR BACTERIAL SURVIVAL AT

TEMPERATURES ANDONE 42 DEGREES CELSIOS.

-I SIMILARITY: CHATAINS 2 PDZ/DHR DOMAINS.
                                                                                                                                                                  Lipinska B., Zylicz M., Georgopoulos C.;
"The HtrA (Degp) protein, essential for Escherichia coli survival at
high temperatures, is an endopeptidase.";
J. Bacteriol. 172:1791-1797(1990).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 PROSITE; PS50106; PDZ; 2.
Hydrolase; Serine protease; Heat shock; Periplasmic; Repeat; Signal;
                                                Wurgler S.M., Richardson C.C.; "Structure and regulation of the gene for dGTP triphosphohydrolase
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    CHARGE RELAY SYSTEM (POTENTIAL)
CHARGE RELAY SYSTEM (POTENTIAL)
CHARGE RELAY SYSTEM (POTENTIAL)
A -> R (IN REF. 1, 7 AND 8).
                                                                                                   Proc. Natl. Acad. Sci. U.S.A. 87:2740-2744(1990).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    PROTEASE DO. PDZ 1. PDZ 2.
                                                                                                                                  CHARACTERIZATION, AND SEQUENCE OF 27-39.
MEDLINE=90202693; PubMed=2180903;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              SWISS-2DPAGE; P09:376; COLI.
BEOGGENE; EG10463; degp.
InterPro; IPR0014'3; PDZ.
InterPro; IPR001940; Protease2C.
InterPro; IPR001213'4; Ser_protease_Try.
Pfam; PF00089; trypsin; 1.
Pfam; PF00089; PDZ; 2.
[8]
SEQUENCE OF 1-16 FROM N.A.
MEDLINE-90207273; PubMed-2157212;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       M36536; AAA:3994.1; -. 1
X42457; CAA:30997.1; -. D26562; BAA05608.1; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     PRINTS; PR00834; PROTEASES2C.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 EMBL, AEOO5192, AAG54465.1;
EMBL, APOO2550; BAB33588.1;
EMBL; M29955. AANTOTOTO
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             AE000125; AAC73272.1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              EMBL, M29955, AAA:3717.1;
EMBL, M31772, AAA:3680.1;
PIR, S01899, S01899.
PIR, B35993; B35993.
MEROPS, S01.273;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           AAB08591.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     131
161
236
10
                                                                                   from Escherichia coli
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      28; PDZ;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Complete proteome
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     131
161
236
10
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      SM002
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      DOMAIN
ACT_SITE
ACT_SITE
ACT_SITE
CONFLICT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      CHAIN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      SMART;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        SIGNAL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             EMBL;
EMBL;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              EMBL;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 MBI
```

```
6
 E -> Q (IN REF. 7).
A -> G (IN REF. 1).
STIYLLMQ -> RHLPVNAVISLNPFLKTGRGSPYNL (IN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ,
S.L.,
                                                                                                                                                                                                                                                                                                                                                                                                              305
                                                                                                                                                                          68 DNLPTIKFSDSNDISVGDLVFAIGNPFGVGESVTQGIVSALNKSGIGINSYENFIQTDAS 127
                                                                                                                                                                                                                                                                                  128 INPGNSGGALIDSRGGLVGINTAIISKTGGNHGIGFAIPSNMVKDTVTQLIKTGKIERGY 187
                                                                                                                              Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Read T.D., Brunham R.C., Shen C., Gill S.R., Heidelberg J.F.,
White O., Hickey E.K., Peterson J., Utterback T., Berry K., Bass S.,
Linher K., Weidman J., Khouri H., Craven B., Bowman C., Dodson R.,
Gwinn M., Nelson W., DeBoy R., Kolonay J., McClarty G., Salzberg S.L.
Eisen J., Fraser C.M.,
                                                                                                                                                          10 ALGSGVIISKD-GYIVTNNHVIDGADKIKVTIPGSNKEYSATLVGTDSESDLAVIRI-TK 67
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 STRAIN=CWL029;
MEDLINE=99206606; PubMed=10192388;
Kalman S., Mitchell W., Marathe R., Lammel C., Fan J., Hyman R.W., Olinger L., Grimwood J., Davis R.W., Stephens R.S.;
"Comparative genomes of Chlamydia pneumoniae and C. trachomatis.";
Nat. Genet. 21:385-389(1999).
                                                                                                                                                                                                                                                                                                                                                LGVGLQDLSGDLQNS--YDNKEGAVVISVEKDSPAKKAGILVWDLITEVNGKKVKNTNEL
                                                                                                                                                                                                                                                                                                                                                                   RNLIGSMLPNQRVTLKVIRDKKERAFTLTLAERKNPNKKETISAQNGAQGQLNGLQVEDL
                                                                                                                                                                                                                                                                                                                                                                                                                            TQETKRSMRLSDDVQGVLVSQVNENSPAEQAGFRQGNIITKIEEVEVKSVADFNHALEKY
                                                                                                                             25;
                                                                                              474;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Genome sequences of Chlamydia trachomatis MoPn and Chlamydia
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           DEGP_CHLPN STANDARD; PRT; 488 AA. 0926T0; 0970D7; 09K1W4; 16-0CT-2001 (Rel. 40, Created) 16-0CT-2001 (Rel. 40, Last sequence update) 15-JUN-2002 (Rel. 41, Last annotation update) 15-JUN-2002 (Rel. 41, Last annotation update) Probable serine protease do-like precursor (EC 3.4.21.-). DEGP OR HTRA OR CPN0979 OR CP0877. Chlamydia pneumoniae (Chlamydophila pneumoniae).
                                                                                              DB 1; Length
                                                                                                                           74; Mismatches 113; Indels
                                                            5482E596F74B6D5F CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Bacteria; Chlamydiales; Chlamydiaceae; Chlamydophila
                                                                                                            Pred. No. 1.6e-35;
                                                                                            37.3%; Score 722.5;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Nucleic Acids Res. 28:1397-1406(2000)
                                               REF. 1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              STRAIN-AR39;
MEDLINE-20150255; PubMed-10684935;
                                                             474 AA; 49354 MW;
                                                                                                                           Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    366 KGKPKRFLVLDLNQG 380
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                [2]
SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      NCBI_TaxID=83558;
   46
192
467
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        AR39.
                                                                                                                           Matches 163;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           pneumoniae
CONFLICT
                                                             SEQUENCE
                                                                                            Query Match
                                CONFLICT
                                                                                                              Best Local
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 DEGP_CHLPN
                                                                                                                                                                                                                                                                                                                                                188
                                                                                                                                                                                                                                                                                                                                                                                                              246
                                                                                                                                                                                                                                                                                                                                                                                                                                                                          306
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ID
DA
DA
DA
DA
DA
DA
DA
NA
OC
OC
 FFFFS
                                                                                                                                                                                                                      δ
                                                                                                                                                                                                                                                  q
                                                                                                                                                                                                                                                                                                                                                                                                                                         g
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     g
                                                                                                                                                          à
                                                                                                                                                                                                                                                                                  ö
                                                                                                                                                                                                                                                                                                               g
                                                                                                                                                                                                                                                                                                                                              ò
                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ð
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    à
```

```
This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (see http://www.isb-sib.ch/announce/or send an email to license@ib-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   7;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ESDLAVIRITKDNLPTIKFSDSNDISVGDLVFAIGNPFGVGESVTQGIVSALNKSGIGIN 116
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  SYENFIQTDASINPGNSGGALIDSRGGLVGINTAIISKTGGNHGIGFAIPSNMVKDTVTQ 176
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            234
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           341
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            NGKKVKNTNELRNLIGSMLPNQRVTLKVIRDKKERAFTLTLAERKNPNKKETISAQNGAQ 294
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      GQLNGLQVEDLTQETKRSMRLSDDVQGVLVSQVNENSPAEQAGFRQGNIITKIEEVEVKS 354
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  26
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Gaps
           MEDLINE-20330349; PubMed-10871362; Shirai M., Hirakawa H., Kimoto M., Tabuchi M., Kishi F., Ouchi K., Shirai M., Hirakawa H., Kimoto M., Ruhara S., Nakazawa T.; Shiba T., Ishii K., Hattori M., Kuhara S., Nakazawa T.; "Comparison of Whole genome sequences of Chlamydia pneumoniae J138 from Japan and CWL029 from USA."; Nucleic Acids Res. 28:2311-2314(2000).
-! SIMILARITY: BELONGS TO PEPTIDASE FAMILY S2C.
-! SIMILARITY: CONTAINS 2 PDZ/DHR DOMAINS.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               222 DFEDEIQTDAAINPGNSGGPLLNIDGQVIGVNTAIVSGSGGYIGIGFAIPSLMANRIIDQ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    2 IPKER-----MERALGSGVIISKDGYIVTNNHVIDGADKIKVTIPGSNKEYSATLVGTDS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           LIRDGOVTRGFLGVTLQPIDAELAACYKLEKVYGALVTDVVKGSPADKAGLKQEDVIIAY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             LIKTGKIERGYLGVGLQDLSGDLQNSY - - DNKEGAVVISVEKDSPAKKAGILVWDLITEV
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        NGKEVDSLSMFRNAVSLMNPDTRIVLKVVREGKVIEIPVTVSQAP---KEDGMSAL----
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Repeat; Signal; Complete proteome.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               POTENTIAL.
PROBABLE SERINE PROTEASE DO-LIKE.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      CHARGE RELAY SYSTEM (POTENTIAL).
CHARGE RELAY SYSTEM (POTENTIAL).
CHARGE RELAY SYSTEM (POTENTIAL).
OEE750P88F106F49 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Length 488;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  37.3%; Score 722.5; DB 1;
40.0%; Pred. No. 1.7e-35;
ive 82; Mismatches 134;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     VADFNHALEKYKGKPKRFLVLDLNQG--YRIILVK 387
                                                                                                                                                                                                                                                                                                                                                              TIGR; CP0877; -...
InterPro; IPR001478; PD2.
InterPro; IPR001249, Protease2C.
InterPro; IPR001254; Ser_protease_Try.
Pfam; PF00089; trypsin; 1.
Pfam; PF00595; PD2; 2.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           CATALYTIC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           PDZ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         = ::
                                                                                                                                                                                                                                                                                EMBL; AE001678; AAD19116.1; -. EMBL; AE002246; AAF38665.1; -. EMBL; AP002548; BAA99186.1; -. MEROPS; S01.273; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Ψ.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                           PRINTS; PRO0834; PROTEASES2C.
SMART; SM00228; PDZ; 2.
PROSITE; PS50106; PDZ; 2.
Hydrolase; Serine protease; F
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       280
372
476
134
164
238
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Conservative
                                                                                                                                                                                                                                                                                                                                                   PHCI-2DPAGE; Q926T0; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      164
238
488 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Similarity
STRAIN-J138
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Best Local Sim
Matches 158;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ACT_SITE
ACT_SITE
ACT_SITE
SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       DOMAIN
DOMAIN
DOMAIN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               SIGNAL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 162
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 57
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                117
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           282
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           235
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          342
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         295
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       395
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       355
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            177
ò
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                g
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ò
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               g
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ò
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            g
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           셤
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ò
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Q
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         à
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       g
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ò
```

us-09-895-913a-120_2.rsp

```
This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
                                                                                                                                                                                                 188 LGVGLQDLSGDLQNS--YDNKEGAVVISVEKDSPAKKAGILVWDLITEVNGKKVKNTNEL 245
                                                                                                                                                                                                                                                                                                                                                                                                                                                306 TQETKRSMRLSDEVQGVLVSQVNENSPAEQAGFRQGNIITKIEEVEVKSVADFNHALEKY 365
                                                                                                                                                                                                                                                                                                                                                                                                                                                             398 IEGAEMSNKGQD--KGVVVSSVKANSPAAQIGLKKGDVIIGANQQPVKNIAELRKILD-- 453
                                                                                                                                                                                                                                                             128 INPGNSGGALIDSRGGLVGINTAIISKTGGNHGIGFAIPSNMVKDTVTQLIKTGKIERGY 187
                                                                                                                                                                                                                                                                                                                                                     292 LGIMGTELNSELAKAMKVDAQRGAFVSQVMPNSSAAKAGIKAGDVITSLNGKPISSFAAL 351
                                                                                                                                                                                                                                                                                                                                                                                     246 RNLIGSMLPNQRVTLKVIRDKKERAFTLTLAERKNPNKKETISAQNGAQGQLNGLQVEDL 305
                                                                                                                                                                                                                                                                                                                                                                                                       Gaps
                                                                                                                                                       10 ALGSGVII-SKDGYIVTNNHVIDGADKIKVTIPGSNKEYSATLVGTDSESDLAVIRI-TK 67
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 30-WAY-2000 (Rel. 39, Created)
30-WAY-2000 (Rel. 39, Last sequence update)
15-JUN-2002 (Rel. 41, Last annotation update)
15-JUN-2002 (Rel. 41, Last annotation update)
Probable serine protease do-like precursor (EC 3.4.21.-).
DEGP OR HIRA.

BIUGELIA abortus.

BACTETIA; Proteobacteria; alpha subdivision; Rhizobiaceae group;
Brucellaceae; Brucella.
                                                                                                         25;
                                                                            DB 1; Length 475;
               (POTENTIAL)
 (POTENTIAL)
                                                                                                         Indels
                                              86E685BF3C1A289F CRC64;
CHARGE RELAY SYSTEM
CHARGE RELAY SYSTEM
CHARGE RELAY SYSTEM
                                                                                          Best Local Similarity 42.9%; Pred. No. 4.9e-35;
Matches 161; Conservative 75; Mismatches 114;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      513 AA
                                                                            Score 714.5;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   MEDLINE=95165990; PubMed=7861951;
                                            49315 MW;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     EMBL; U07352; AAA70164.1; -.
                                                                            36.98;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  InterPro; IPR001478; PDZ.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             366 KGKPKRFLVLDLNQG 380
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          454 -SKPS-VLALNICRG 466
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        STANDARD;
132
162
237
475 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         NCBI_TaxID=235;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      STRAIN=2308
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      DEGP_BRUAB
Q44597;
ACT_SITE
ACT_SITE
                              ACT_SITE
SEQUENCE
                                                                              Query Match
 SFFF
                                                                                                                                                                                                                                                                                                                                                                                                                                                                             g
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ŏ
                                                                                                                                                                      ద
                                                                                                                                                                                                    ð
                                                                                                                                                                                                                               qq
                                                                                                                                                                                                                                                             δ
                                                                                                                                                                                                                                                                                          g
                                                                                                                                                                                                                                                                                                                        à
                                                                                                                                                                                                                                                                                                                                                     g
                                                                                                                                                                                                                                                                                                                                                                                     à
                                                                                                                                                                                                                                                                                                                                                                                                                                               δ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ò
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        g
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the Buropean Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/
                                                                                                                                                                                                                                                                                                                                                                                             SEQUENCE FROM N.A.

STRAIN-LIZ / SGS1412 / ATCC 700720;

MEDLINE-21534948; PubMed=11677609;

MCDLINE-21534948; PubMed=11677609;

MCDLIAnd M., Sanderson K.E., Spieth J., Clifton S.W., Latreille P., Courtney L., Porwollik S., Ali J., Dante M., Du F., Hou S., Layman D., Leonard S., Mauyen C., Scott K., Holmes A., Grewal N., Mulvaney E., Ryan E., Sun H., Florea L., Miller W., Stoneking T., Nhan M., Waterston R., Wilson R.K.;

"Complete genome sequence of Salmonella enterica serovar Typhimurium
                                                                                                                                                                                                                                                                                        MEDLINE=91251770; PubMed=1645840;
Johnson K., Charles I., Dougan G., Pickard D., O'Gaora P., Costa G.,
Ali T., Miller I., Hormacche C.;
"The role of a stress-response protein in Salmonella typhimurium
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Heat shock; Periplasmic; Repeat; Signal;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Nature 413:852-856(2001).
-i- FUNCTION: SERINE PROTEASE THAT IS REQUIRED AT HIGH TEMPERATURE.
INVOLVED IN THE DEGRADATION OF DAMAGED PROTEINS. SHARED
SPECIFICITY WITH HHOA/DEGO.
                                                                                                                                                                                    -:- SUBCELLULAR LOCATION: Periplasmic.
-:- INDUCTION: BY HEAT SHOCK.
-:- SIMILARITY: BELONGS TO PEPTIDASE FAMILY S2C.
-:- SIMILARITY: CONTAINS 2 PDZ/PHR DOMAINS.
                                                                                                                      Ol-AUG-1992 (Ref. 23, Last sequence update)
15-JUN-2002 (Rel. 41, Last annotation update)
15-GOV (Res. 41, Last annotation update)
DEGP OR HTRA OR PTD OR STM0209.
454 IEDLNRTL---KDSNNENILLMVSQGDVIRFIALK 485
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  BY SIMILARITY.
PROTEASE DO.
PDZ 1.
PDZ 2.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       or send an email to license@isb-sib.ch)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       nterPro; IPR001254; Ser_protease_Try.
                                                                                                                                                                                                                                                                                                                                                                    Mol. Microbiol. 5:401-407(1991).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          InterPro; IPR001478; PDZ.
InterPro; IPR001940; Protease2C.
                                                                                                         23, Created)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              EMBL; AE008704; AAL19173.1; -. PIR; S1537; S1537; S1537. PIR; S21327; MEROPS; S01.273; -. StyGene; S010173; degp.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       PRINTS; PR00834; PROTEASES2C
SMART; SM00228; PDZ; 2.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Hydrolase; Serine protease;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    EMBL; X54548; CAA38420.1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Pfam; PF00089; trypsin; 1
Pfam; PF00595; PDZ; 2.
                                                                           STANDARD;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     26
475
372
467
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       PROSITE; PS50106; PDZ;
                                                                                                                                                                                                                                                             SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Complete proteome.
                                                                                                    01-AUG-1992 (Rel/
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  27
281
378
                                                                                                                                                                                                                             NCBI_TaxID=602;
                                                                           DEGPSALTY
                                                                                                                                                                                                                 Salmonella.
                                                                                                                                                                                                                                                                                                                                                       virulence.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  DOMAIN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       SIGNAL
                                                            DEGP_SALTY
                                            RESULT 5
a
```

```
CHAIN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       182
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            298
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 388
       RRAPA
RRAPA
RRAPA
RAPA
REFFFFFFFFFFF
FFFFFFFFFFFFFFFFF
SOT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               g
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        g
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           à
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     õ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ò
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  a
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           a
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  à
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      셤
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ò
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                g
                                                                                                                                                                                                                         . 7;
                                                                                                                                                                                                                                                                                          118
                                                                                                                                                                                                                                                                                                    422
                                                                                                                                                                                                                                                                                                                                                                                                                                                                          119 ENFIQTDASINPGNSGGALIDSRGGLVGINTAIISKTGGNHGIGFAIPSNMVKDTVTQLI 178
                                                                                                                                                                                                                                                                                                                                                                            179 KTGKIERGYLGVGLQDLSGDLQNSYD--NKEGAVVISVEKDSPAKKAGILVWDLITEVNG 236
                                                                                                                                                                                                                                                                                                                                                                                                                      237 KKVKNTNELRNLIGSMLPNQRVTLKVIRDKKERAFTLTLAERKNPNKKETISAQNGAQGQ 296
                                                                                                                                                                                                                                                                                                                                                                                                                                                               297 LNGLQVEDLTQETKRSMRLSDDVQGVLVSQVNENSPAEQAGFRQGNIITKIEEVEVKSVA 356
                                                                                                                                                                                                                          Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         SEQUENCE FROM N.A.

STRAIN=Rd / KW20 / ATCC 51907;

MEDLINE=95350630; PubMed=7542800;

Fleischmann R.D., Adams M.D., White O., Clayton R.A., Kirkness E.F.,

Kerlavage A.R., Bult C.J., Tomb J.-F., Dougherty B.A., Merrick J.M.,

McKenney K., Sutton G., Fitzhugh W., Fields C.A., Gocayne J.D.,

Scott J.D., Shirley R., Liu L.-I., Glodek A., Kelley J.M.,
                                                                                                                                                                                                                                              3 PKERMER--ALGSGVIISKDGYIVTNNHVIDGADKIKVTIPGSNKEYSATLVGTDSESDL 60
                                                                                                                                                                                                                                                                                                                                                                                                                                    : |: : : | : : | | | | : : | | | : : | 363 ETVQDPRDLARKVANIAPGEKAALTVWRKNRAEEINVTIAAMPNDKGKSGSQSNDNDGGQ
                                                                                                                                                                                                                                                                                        61 AVIRIT -- KDNLPTIKFSDSNDISVGDLVFAIGNPFGVGESVTQGIVSALNKSGIGINSY
                                                                                                                                                                                                                          27;
                                                                                           POTENTIAL.
PROBABLE SERINE PROTEASE DO-LIKE.
CATALYTIC.
                                                                                                                                             CHARGE RELAY SYSTEM (POTENTIAL).
CHARGE RELAY SYSTEM (POTENTIAL).
CHARGE RELAY SYSTEM (POTENTIAL).
                                                                                                                                                                                                   ; Score 679.5; DB 1; Length 513;
; Pred. No. 6e-33;
64; Mismatches 150; Indels 27
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Bacteria; Proteobacteria; gamma subdivision; Pasteurellaceae;
Haemophilus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 HTOA_HAEIN STANDARD; PRT; 466 AA.
P45129;
01-NOV-1995 (Rel. 32, Created)
01-NOV-1995 (Rel. 32, Last sequence update)
15-JUN-2002 (Rel. 41, Last annotation update)
Probable periplasmic serine protease do/hhoA-like precursor
                                                                                Periplasmic; Repeat; Signal
                                                                                                                                                                               DEICEF1959472806 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          DFNHA------379
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              477 DINKAITAAEKSGRKAVLLQLQSNDQSRFVALPINQ 512
InterPro; IPR001940; Protease2C.
InterPro; IPR001254; Ser_protease_Try.
Pfam; PF00089; trypsin; 1.
Pfam; PF000595; PDE; 2.
PRINTS; PR00834; PROTEASES2C.
SMART; SM00228; PDE; 2.
PROSITE; PS50106; PDZ; 2.
PROSITE; PS50106; PDZ; 2.
                                                                                                                                                                               53483 MW;
                                                                                                                                                                                                   35.18;
39.18;
                                                                                                                                                                                                             Best Local Similarity 39.19
Matches 155; Conservative
                                                                                                                         391
500
152
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Haemophilus influenzae
                                                                                                                                   414
152
182
182
257
513 AA;
                                                                                                               125
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      NCBI_TaxID=727;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  (EC 3.4.21.-).
                                                                                                              DOMAIN
DOMAIN
DOMAIN
ACT_SITE
ACT_SITE
ACT_SITE
                                                                                                                                                                                                    Query Match
                                                                                         SIGNAL
                                                                                                      CHAIN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         OA_HAEIN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         357
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              RESULT 7
     g
                                                                                                                                                                                                                                                                                                                                                        g
                                                                                                                                                                                                                                                                                                                                                                                               g
                                                                                                                                                                                                                                                                                                                                                                                                                      õ
                                                                                                                                                                                                                                                                                                                                                                                                                                         g
                                                                                                                                                                                                                                                                                                                                                                                                                                                               ò
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     g
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             g
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 à
                                                                                                                                                                                                                                                                                                                                  õ
                                                                                                                                                                                                                                                                                                                                                                           à
```

```
This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        9
                                                                                                                                  Whole-genome random sequencing and assembly of Haemophilus influenzae
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     214
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                64 RITK-DNLPTIKFSDSNDISVGDLVFAIGNPFGVGESVTQGIVSALNKS-GIGINSYENF 121
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             122 IQTDASINPGNSGGALIDSRGGLVGINTAIISKTGGNHGIGFAIPSNMVKDTVTQLIKTG 181
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      334
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        240 KNTNELRNLIGSMLPNQRVTLKVIRDKKERAFTLTLA--ERKNPNKKETISAQNGAQGQL 297
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             387
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  NGLQVEDLTQETKRSMRLSDDVQGVLVSQVNENSPAEQAGFRQGNIITKIEEVEVKSVAD 357
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          5 ERMERALGSGVII-SKDGYIVTNNHVIDGADKIKVTIPGSNKEYSATLVGTDSESDLAVI 63
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Gaps
Weidman J.F., Phillips C.A., Spriggs T., Hedblom E., Cotton M.D., Utterback T.R., Hanna M.C., Nguyen D.T., Saudek D.M., Brandon R.C. Fritchman J.L., Fuhrmann J.L., Geoghagen N.S.M., Gnehm C.L., McDonald L.A., Small K.V., Fraser C.M., Smith H.O.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               KIERGYLGVGLQDLSGDLQNSYD--NKEGAVVISVEKDSPAKKAGILVWDLITEVNGKKV
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             SSFAEIRAKIATTGAGKEISLTYLRDGKSHDVKMKLQADDSSQLSSKTELPA----L
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         PROBABLE PERIPLASMIC SERINE PROTEASE DO/HHOA-LIKE.
                                                                                                                                                                                                                                            BETWEEN E.COLI
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Indels 24;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                120 CHARGE RELAY SYSTEM (POTENTIAL).
120 CHARGE RELAY SYSTEM (POTENTIAL).
226 CHARGE RELAY SYSTEM (POTENTIAL).
49434 MM; ED050A00047B5851 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Length 466;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Periplasmic; Repeat; Signal;
                                                                                                                                                                                  Science 269:496-512(1995).
-!- SUBCELLULAR LOCATION: Periplasmic (Potential)
-!- SIMILARITY: SEEMS TO BE A INTERMEDIATE FORMS !
(PROTEASE DO) AND HHOA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                35.0%; Score 679; DB 1; L/41.3%; Pred. No. 5.7e-33; ive 76; Mismatches 115;
                                                                                                                                                                                                                                                                                              -!- SIMILARITY: BELONGS TO PEPTIDASE FAMILY S2C. -!- SIMILARITY: CONTAINS 2 PDZ/DHR DOMAINS.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             InterPro; IPR001478; PD2.
InterPro; IPR001940; Protease2C.
InterPro; IPR001254; Ser_protease_Try.
Pfam; PF00089; trypsin; 1.
Pfam; PF00595; PD2; 2.
PRINTS; PR00834; PROTEASES2C.
SMART; SM00228; PD2; 2.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      POTENTIAL.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 PDZ 1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               EMBL; U32805; AAC22906.1; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Hydrolase; Serine protease;
Complete proteome.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Best Local Similarity 41.3%
Matches 151; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      29
466
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        PROSITE; PS50106; PDZ;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                120
150
226
466 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        MEROPS; S01.274;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            30
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    TIGR; HI1259;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ACT_SITE
ACT_SITE
ACT_SITE
SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 DOMAIN
DOMAIN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      SIGNAL
```

```
LQVEDLTQETKREMRLSDDVQGVLVSQVNENSPAEQAGFRQGNIITKIEEVEVKSVADFN 359
           182 KIERGYLGVGLQCLSGDLQN--SYDNKEGAVVISVEKDSPAKKAGILVWDLITEVNGKKV 239
                                                                 KNTNELRNLIGSMLPNQRVTLKVIRDKKERAFTLTLAERKNPNKKETISAQNGAQGQLNG
                                                                                                                                                         360 HALEKYKGKPKRF'LVLDLNQG 380
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     134
164
242
508 AA;
                                                                                                                                                                                                                                                                                                                                              [1]
SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Query Match
Best Local Similarity
                                                                                                                                                                                                                                                                                                   Rickettsia conorii
                                                                                                                                                                                                                                                                                                                                   NCBI_TaxID=781;
                                                                                                                                                                                                                       DEGP_RICCN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           PROSITE; PS
Hydrolase;
                                                                                                                                                                                                                                                                                                                                                                                                           Raoult D.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           CHAIN
DOMAIN
DOMAIN
DOMAIN
ACT_SITE
ACT_SITE
ACT_SITE
SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                SIGNAL
                                                      240
                                                                                                 300
                                                                                                                                                                                                   RESULT
                               В
                                                                        g
                                                                                                ŏ
                                                                                                                     g
                                                                                                                                                              g
                                                                                                                                                                                                                         ŏ
                                                    ŏ
                                                                                                                                            å
                                                                                                                                                                                                                                                                                                                     This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation - the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is no way modifited and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     8;
                                                                                                                                                      Buchnera aphidicola (subsp. Acyrthosiphon pisum) (Acyrthosiphon pisum
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        121
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          IQLKNANNLSEIKIADSDNLRVGDYTVAIGNPYGLGETVTSGIISALGRSGLNIEHYENF 226
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             IQTDASINPGNSGGALIDSRGGLVGINTALISKTGGNHGIGFAIPSNAVKDTVTQLIKTG 181
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    IRI-TKDNLPTIKFSDSNDISVGDLVFAIGNPFGVGESVTQGIVSALNKSGIGINSYENF
|:: :|| || :||:|| || ||||||
                                                                                                                                                                                                                                        Shigenobu S., Watanabe H., Hattori M., Sakaki Y., Ishikawa H.;
"Genome sequence of the endocellular bacterial symbiont of aphids buchnera sp. APS.";
Nature 407:81-86(2006)
-:- SIMILARITY: BELONGS TO PEPTIDASE FAMILY S2C.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Repeat; Signal; Complete proteome. POTENTIAL.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             PROBABLE SERINE PROTEASE DO-LIKE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        CHARGE RELAY SYSTEM (POTENTIAL).
CHARGE RELAY SYSTEM (POTENTIAL).
REBREAY SYSTEM (POTENTIAL).
868E8732CAC50629 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               DB 1; Length 478;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Indels
                                                                                                                               Probable serine protease do-like precursor (EC 3.4.21.-).
DEGP OR BU228.
                                                                                                                                                             symbiotic bacterium).
Bacteria; Proteobacteria; gamma subdivision; Buchnera.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              35.0%; Score 678.5; DB 1;
llarity 39.4%; Pred. No. 6.3e-33;
Conservative 89; Mismatches 119;
                                                                                              16-OCT-2001 (Rel. 40, Created)
16-OCT-2001 (Rel. 40, Last sequence update)
15-JUN-2002 (Rel. 41, Last annotation update)
                                                                          478 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                    MEROPS; S01.273; -.
InterPro; IPR001478; PDZ.
InterPro; IPR00149; Protease2C.
InterPro; IPR001940; Protease_Try.
Pfam; PF00089; trypsin; 1.
Pfam; PF00089; trypsin; 1.
PRINTS; PR00844; PROTEASES2C.
SMART; SM00228; PDZ; 2.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          CATALYTIC.
                                                                                                                                                                                                          SEQUENCE FROM N.A.
STRAIN-TOKYO 1998;
MEDLINE-20445173; PubMed=10993077;
                                                                                                                                                                                                                                                                                                                                                                                                           EMBL; AP001118; BAB12943.1; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        52230 MW;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Serine protease;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            PS50106; PDZ; 1.
                                                                          STANDARD;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  163
238
478 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Best Local Similarity
Matches 150; Conserv
                                                                                                                                                                                     NCBI_TaxID=118099
358 FNHALE 363
                   439 LNKVLE 444
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Hydrolase;
                                                                          DEGP_BUCAI
P57322;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ACT_SITE
ACT_SITE
ACT_SITE
SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            PROSITE;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      DOMAIN
DOMAIN
DOMAIN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    SIGNAL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             CHAIN
                                                               DEGP_BUCAI
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                108
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      227
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           167
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     63
                                                                          엽
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Q
à
                   셤
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ò
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          윱
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ö
```

```
This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bloinformatics and the EMBL outstation the European Bloinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Ogata H., Audic S., Renesto-Audiffren P., Fournier P.-E., Barbe V., Samson D., Roux V., Cossart P., Weissenbach J., Claverie J.-M.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       "Mechanisms of evolution in Rickettsia conorii and R. prowazekii.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              PS50106; PDZ; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           PROBABLE SERINE PROTEASE DO-LIKE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     CHARGE RELAY SYSTEM (POTENTIAL).
CHARGE RELAY SYSTEM (POTENTIAL).
CHARGE RELAY SYSTEM (POTENTIAL).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Length 508;
                                                                                                                                                                                                                                                    Bacteria; Proteobacteria; alpha subdivision; Rickettsiales;
                                                                                     15-JUN-2002 (Rel. 41, Last sequence update)
15-JUN-2002 (Rel. 41, Last annotation update)
Probable serine protease do-like precursor (EC 3.4.21.-).
DEGP OR HTRA OR RC0166.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           D2F53A690ECD0AD7 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Score 663.5; DB 1;
Pred. No. 5.1e-32;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Science 293:2093-3098(2001).
-i- SIMILARITY: BELONGS TO PEPTIDASE FAMILY S2C.
-i- SIMILARITY: CUNTAINS 2 PDZ/DHR DOMAINS.
                                                                                                                                                                                                                                                                                     Rickettsiaceae; Rickettsieae; Rickettsia
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               CATALYTIC.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                EMBL; AE008583; AAL02704.1; ALT_INIT.
InterPro; IPR001478; PDZ.
InterPro; IPR001940; Protease2C.
InterPro; IPR001254; Ser_protease_Try.
Pfam; PF00089; trypsin; 1.
Pfam; PF00595; PDZ; 2.
                                                                                                                                                                                                                                                                                                                                                                                                                  STRAIN=Malish 7;
MEDLINE=21442074; PubMed=11557893;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             PDZ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       242 CF
55599 MW;
                                                 15-JUN-2002 (Rel. 41, Created)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   PRINTS; PR00834; PROTEASES2C. SMART; SM00228; PDZ; 2.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          34.2%;
STANDARD;
```

```
01-FEB-1995 (Rel. 31, Created)
01-FEB-1995 (Rel. 31, Last sequence update)
15-JUN-2002 (Rel. 41, Last annotation update)
DEGO OR HHOA OR B3234.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         455 AA.
                                                                                                                                       33.9%; Score 657.5; 39.4%; Pred. No. 1.1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        SEQUENCE FROM N.A., AND SEQUENCE OF 28-32.
              PROBABLE SEI
CATALYTIC.
PDZ 1.
PDZ 2.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     STRAIN-K12 / W3110;
MEDLINE-96165272; PubMed-8576051;
Waller P.R., Sauer R.T.;
"Characterization of degQ and degS, I
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             mologs of the DegP protease.";
Bacteriol. 178:1146-1153(1996)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                SEQUENCE FROM N.A.
STRAIN-K12 / MG1655;
MEDLINE-97426617; PubMed-9278503;
                                                                                                            51303 MW;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           365 YKGKPKRFLVLDLNQG 380
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      457 --SKP-NILVFSVKRG 469
                                                                                                                                                                  Matches 148; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         STANDARD;
 26
478
372
469
1133
238
                           116
281
387
133
163
238
478 AA;
                                                                                                                                                       Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Escherichia coli.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Escherichia.
NCBI_TaxID=562;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         DEGO_ECOLI
                                                                  ACT_SITE
ACT_SITE
ACT_SITE
                                                                                                               SEQUENCE
                                                                                                                                        Query Match
                                                                                                                                                       Local
                                         DOMAIN
                                                        DOMAIN
                                                                                                                                                                                                                                                                                                                                                                                                                 246
                                                                                                                                                                                                                                                                                                                                                           188
                                                                                                                                                                                                                                                                                                                                                                                                                                                                      305
                                                                                                                                                       Best
    g
                                                                                                                                                                                                                                                                                                                                qq
                                                                                                                                                                                                                                                                                                                                                                                                                                           g
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                g
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       à
                                                                                                                                                                                                                                                                           g
                                                                                                                                                                                                                                                                                                      ö
                                                                                                                                                                                                                                                                                                                                                             ò
                                                                                                                                                                                                                                                                                                                                                                                   QQ
                                                                                                                                                                                                                                                                                                                                                                                                                 ð
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            à
                                                                                                                                                                                                                                                                                                                                                                                                                                                                      õ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bloinformatics and the EMBL outstation the European Bloinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
  9
                                                                                                | : :||:| : : | |::: ::| |:: : | 415 SITKNNITFGNLTEELRQKYIPQDKMGIVITNIDE----EESSFRIGDLITNINQKSID 470
                                          126 ASINPGNSGGALIDSRGGLVGINTAIISKTGGNHGIGFAIPSNMVKDTVTQLIKTGKIER 185
                                                                                                                                                       186 GYLGVGLQDLSGDLQN--SYDNKEGAVVISVEKDSPAKKAGILVWDLITEVNGKKVKNTN 243
                                                                                                                                                                                                             244 ELRNLIGSMLPNQRVTLKVIRDKKERAFTL-----TLAERKNPNKKE-TISAQNGA 293
                                                                                                                                                                                                                                                                 :|| :| :| :| | :||||| : | :||||| 355 KLRVIIADAPIDQEVKVKILRDKKELELPIKITSDNEEVTKDSTEETNKKEITNKEENNL 414
                                                                                                                                                                                                                                                                                                      294 QGQLNGLQVEDLTQETKRSMRLSDDVQGVLVSQVNENSPAEQAGFRQGNIITKIEEVEVK 353
                                                                                  LPTIKFSDSNDISVGDLVFAIGNPFG-VGESVTQGIVSALNKSGIGI----NSYENFIQTD 125
  Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Thao M.L., Baumann P.; "Sequence analysis of a DNA fragment from Buchnera aphidicola (Aphid endosymbiont) containing the genes dapD-htrA-llvI-llvH-ftsL-ftsI-
                             LGSGVIISKDGYIVTNNHVIDGADKIKVTIPGSNKEYSATLVGTDSESDLAVIRI-TKDN 69
 23;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                16-OCT-2001 (Rel. 40, Created)
16-OCT-2001 (Rel. 40, Last sequence update)
15-JUN-2002 (Rel. 41, Last annotation update)
Probable serine protease do-like precursor (EC 3.4.21.-).
  Mismatches 139; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Buchnera aphidicola (subsp. Schizaphis graminum).
Bacteria; Proteobacteria; gamma subdivision; Buchnera.
NCBI_TaxID=98794;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Curr. Microbiol. 37:214-216(1998).
-!- SIMILARITY: BELONGS TO PEPTIDASE FAMILY S2C.
-!- SIMILARITY: CONTAINS 2 PDZ/DHR DOMAINS.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    MEROPS; S01.273; -...
InterPro; IPR001478; PDZ.
InterPro; IPR001940; Protease2C.
InterPro; IPR001254; Ser_protease_Try.
Pfam; PF00089; trypsin, 1...
Pfam; PF00595; PDZ; 2.
PRINTS; PR00844; PROTEASES2C.
SMART; SM00228; PDZ; 2.
PROSITE; PS50106; PDZ; 1...
Hydrolase; Serine protease; Repeat; Signal.
                                                                                                                                                                                                                                                                                                                                                                                                                                                        478 AA
                                                                                                                                                                                                                                                                                                                                                                           :: | | | :::| ::|
471 DISKLEELYENAKKSDKKNILLLIERG 497
                                                                                                                                                                                                                                                                                                                                                           354 SVADFNHALEKYKGKPKRFLVLDLNQG 380
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      SEQUENCE FROM N.A.
MEDLINE-98353428; Pubmed-9688822;
72;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          EMBL; AF060492; AAC32331.1; -.
  Matches 153; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                         STANDARD;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         DEGP OR HTRA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                        DEGP_BUCAP
085291;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             murE."
                                                      117
                                                                                 70
                                                                                                                                                                                                                                                                                                                                                                                                                              RESULT 10
                                                                                                                                                                                                                                                                                                                                                                                   g
                                                                                                                                                                                                                                                                                                                                                                                                                                                                     셤
                                                                                                          a
                                                                                                                                       ð
                                                                                                                                                               셤
                                                                                                                                                                                         ò
                                                                                                                                                                                                                  a
                                                                                                                                                                                                                                                ò
                                                                                                                                                                                                                                                                          셤
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  à
                                                                                                                                                                                                                                                                                                      à
```

```
10;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              245
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            173 KNLSAIKIADSDTLRVGDYTVAIGNPYGLGETVTSGIISALGRSGLNIEHYENFIQTDAA 232
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       128 INPGNSGGALIDSRGGLVGINTAIISKTGGNHGIGFAIPSNMVKDTVTQLIKTGKIERGY 187
                                                                                                                                                                                                                                                                                                                                                                                             68 DNLPTIKFSDSNDISVGDLVFAIGNPFGVGESVTQGIVSALNKSGIGINSYENFIQTDAS 127
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   LTQETKRSMRLSDDVQGVLVSQVNENSPAEQAGFRQGNIITKIEEVEVKSVADFNHALEK 364
                                                                                                                                                                                                                                                         Gaps
                                                                                                                                                                                                                                                                                                    10 ALGSGVIISKD-GYIVTNNHVIDGADKIKVTIPGSNKEYSATLVGTDSESDLAVIRI-TK 67
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Escherichia coli genes encoding
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          RNLIGSMLPNORVTLKVIRDKKERAFTLTLAERKNPNKKETISAONGAOGOL-NGLOVED
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 LGVGLQDLSGDLQN--SYDNKEGAVVISVEKDSPAKKAGILVWDLITEVNGKKVKNTNEL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Bacteria; Proteobacteria; gamma subdivision; Enterobacteriaceae;
                                                                                                                                                                                                                                                       25;
SERINE PROTEASE DO-LIKE.
                                                                                        CHARGE RELAY SYSTEM (POTENTIAL).
CHARGE RELAY SYSTEM (POTENTIAL).
CHARGE RELAY SYSTEM (POTENTIAL).
CHARGE ASLAY FEFABSBE CRC64;
                                                                                                                                                                                                            Length 478;
                                                                                                                                                                                                                                                         Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   SECUENCE FROM N.A.
STRAIN-K12 / W3110;
Bass S., Gu Q., Goddard A.;
Submitted (OCT-1994) to the EMBL/GenBank/DDBJ databases.
                                                                                                                                                                                                                                                    82; Mismatches 121;
                                                                                                                                                                                                            DB 1;
                                                                                                                                                                                                                                      Pred. No. 1.1e-31;
```

σ

357 DFNH------ALEKYKGKPKRFLVL 375

ò

```
This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (see http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      8
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    62 VIRI-TKDNLPTIKFSDSNDISVGDLVFAIGNPFGVGESVTQGIVSALNKSGIGINSYEN 120
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            121 FIQIDASINPGNSGGALIDSRGCLVGINTAIISKTGGNHGIGFAIPSNMVKDTVTQLIKT 180
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             GKIERGYLGVGLQDLSGDLQNSY - - DNKEGAVVISVEKDSPAKKAGILVWDLITEVNGKK 238
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            VKNTNELRNLIGSMLPNQRVTLKVIRDKK--ERAFTLTLAERKNPNKKETISAQNGAQGQ 296
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      LNSFAELRSRIATTEPGTKVKLGLLRNGKPLEVEVTLDTSTSSSASAEMITPALEGA--- 378
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     LNGLOVEDLTQETKRSMRLSDDVQGVLVSQVNENSPAEQAGFRQGNIITKIEEVEVKSVA 356
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    32; Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   3 PKERMERALGSGVII-SKDGYIVTNNHVIDGADKIKVTIPGSNKEYSATLVGTDSESDLA 61
Blattner F.R., Plunkett G. III, Bloch C.A., Perna N.T., Burland V., Riley M., Collado-Vides J., Glasner J.D., Rode C.K., Mayhew G.F., Gregor J., Davis N.W., Kirkpatrick H.A., Goeden M.A., Rose D.J., Mau B., Shao Y.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  -i- FUNCTION: PROTEASE WITH A SHARED SPECIFICITY WITH DEGP/DEGP.
-i- SUBCELLULAR LOCATION: Periplasmic.
-i- SIMILARITY: BELONGS TO PEPTIDASE FAMILY S2C.
-i- SIMILARITY: CONTAINS 2 PDZ/DHR DOMAINS.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      CHARGE RELAY SYSTEM (POTENTIAL).
CHARGE RELAY SYSTEM (POTENTIAL).
CHARGE RELAY SYSTEM (POTENTIAL).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Length 455;
                                                                 "The complete genome sequence of Escherichia coli K-12."; Science 277:1453-1474(1997).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   33.6%; Score 652; DB 1; Length 45:
38.7%; Pred. No. 2.1e-31;
-1ve 76; Mismatches 130; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             PRINTS; PR00834; PROTEASES2C.
SMARY; SM00228; PDZ; 2.
PROSITE; PS20106; PDZ; 2.
Hydrolase; Serine protease; Periplasmic; Repeat; Signal;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      6A090F93AC021C83 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              PROTEASE DEGQ.
                                                                                                                                                                                                                                                                                                                                                                                              EcoGene; EG12612, dego.
InterPro; IPR001478; PDZ.
InterPro; IPR001940; Protease2C.
InterPro; IPR001254; Ser_protease_Try.
Pfam; PF00089; trypsin; 1.
Pfam; PF00595; PDZ; 2.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        47205 MW;
                                                                                                                                                                                                                                                                                                      EMBL; U15661; AAC43992.1; -.
                                                                                                                                                                                                                                                                                                                     U32495; AAC44005.1; -. U18997; AAA58036.1; -.
                                                                                                                                                                                                                                                                                                                                               EMBL; AE000402; AAC76266.1;
                                                                                                                                                                                                                                                                                                                                                                  MEROPS; S01.274; -. SWISS-2DPAGE; P39099; COLI.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Matches 150; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            27
349
447
1109
1139
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         258
355
109
139
214
455 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Complete proteome.
                                                                                                                                                                                                                                                                                                                                     EMBL; U18997
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ACT_SITE
ACT_SITE
ACT_SITE
SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           DOMAIN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               SIGNAL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             DOMAIN
                                                                                                                                                                                                                                                                                                                        EMBL:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           202
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          181
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        262
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         239
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    379
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    322
    g
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ò
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                à
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             g
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ò
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          셤
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          õ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     g
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       à
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    a
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               셤
```

```
This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Andersson J.O., Andersson S.G.E.;
"Genomic rearrangements during evolution of the obligate intracellular parasite Rickettsia prowazekii as inferred from an analysis of 52015 bp nucleotide sequence.";
Microbiology 143:2783-2795(1997).
-!- SIMILARITY: BELONGS TO PEPTIDASE FAMILY S2C.
-!- SIMILARITY: CONTAINS 2 PDZ/DHR DOMAINS.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               6
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Andersson S.G.E., Zomorodipour A., Andersson J.O., Sicheritz-Ponten I., Alsmark U.C.M., Podowski R.M., Naeslund A.K., Eriksson A.-S., Winkler H.H., Kurland C.G.; "The genome sequence of Rickettsia prowazekii and the origin of mitochondria.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            23;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  POTENTIAL.
PROBABLE SERINE PROTEASE DO-LIKE.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Signal; Complete proteome.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Length 513;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       CHARGE RELAY SYSTEM (POTENTIAL).
CHARGE RELAY SYSTEM (POTENTIAL).
CHARGE RELAY SYSTEM (POTENTIAL).
                                                                                                                                                                                                                                                                                                                                                                            Bacteria; Proteobacteria; alpha subdivision; Rickettsiales;
Rickettsiaceae; Rickettsieae; Rickettsia.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Indels
                                                                                                                                                                                               16-OCT-2001 (Rel. 40, Created)
16-OCT-2001 (Rel. 40, Last sequence update)
15-UNA-2002 (Rel. 41, Last annotation update)
Probable serine protease do-like precursor (EC 3.4.21.-).
DEGP OR HTRA OR RP124.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 4B7E9B7AB4079139 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ; Score 625.5; DB 1;
; Pred. No. 8.8e-30;
79; Mismatches 139;
                                                                                                                                                         513 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               CATALYTIC.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      InterPro; IPR001478; PDZ.
InterPro; IPR001940; Protease2C.
InterPro; IPR0012354; Ser_protease_Try.
Pfam; PF00089; trypsin; 1.
Pfam; PF00595; PDZ; 1.
: :| :: :| ... :| ... :| ... :| ... :| ... :| ... :| ... :| ... :| ... :| ... :| ... :| ... :| ... :| ... :| ... :| ... :| ... :| ... :| ... :| ... :| ... :| ... :| ... :| ... :| ... :| ... :| ... :| ... :| ... :| ... :| ... :| ... :| ... :| ... :| ... :| ... :| ... :| ... :| ... :| ... :| ... :| ... :| ... :| ... :| ... :| ... :| ... :| ... :| ... :| ... :| ... :| ... :| ... :| ... :| ... :| ... :| ... :| ... :| ... :| ... :| ... :| ... :| ... :| ... :| ... :| ... :| ... :| ... :| ... :| ... :| ... :| ... :| ... :| ... :| ... :| ... :| ... :| ... :| ... :| ... :| ... :| ... :| ... :| ... :| ... :| ... :| ... :| ... :| ... :| ... :| ... :| ... :| ... :| ... :| ... :| ... :| ... :| ... :| ... :| ... :| ... :| ... :| ... :| ... :| ... :| ... :| ... :| ... :| ... :| ... :| ... :| ... :| ... :| ... :| ... :| ... :| ... :| ... :| ... :| ... :| ... :| ... :| ... :| ... :| ... :| ... :| ... :| ... :| ... :| ... :| ... :| ... :| ... :| ... :| ... :| ... :| ... :| ... :| ... :| ... :| ... :| ... :| ... :| ... :| ... :| ... :| ... :| ... :| ... :| ... :| ... :| ... :| ... :| ... :| ... :| ... :| ... :| ... :| ... :| ... :| ... :| ... :| ... :| ... :| ... :| ... :| ... :| ... :| ... :| ... :| ... :| ... :| ... :| ... :| ... :| ... :| ... :| ... :| ... :| ... :| ... :| ... :| ... :| ... :| ... :| ... :| ... :| ... :| ... :| ... :| ... :| ... :| ... :| ... :| ... :| ... :| ... :| ... :| ... :| ... :| ... :| ... :| ... :| ... :| ... :| ... :| ... :| ... :| ... :| ... :| ... :| ... :| ... :| ... :| ... :| ... :| ... :| ... :| ... :| ... :| ... :| ... :| ... :| ... :| ... :| ... :| ... :| ... :| ... :| ... :| ... :| ... :| ... :| ... :| ... :| ... :| ... :| ... :| ... :| ... :| ... :| ... :| ... :| ... :| ... :| ... :| ... :| ... :| ... :| ... :| ... :| ... :| ... :| ... :| ... :| ... :| ... :| ... :| ... :| ... :| ... :| ... :| ... :| ... :| ... :| ... :| ... :| ... :| ... :| ... :| ... :| ... :| ... :| ... :| ... :| ... :| ... :| ... :| ... :| ... :| ... :| ... :| ... :| ... :| ... :| ... :| ... :| ... :| ... :| ... :| ... :
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Repeat;
                                                                                                                                                         PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    STRAIN=Madrid E;
MEDLINE=99039499; PubMed=9823893;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       STRAIN=Madrid E;
MEDLINE=97419517; Pubmed=9274032;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           EMBL; AJ235270; CAA14593.1; -. EMBL; Y11782; CAA72471.1; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 56309 MW;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                SEQUENCE OF 161-513 FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    PRINTS; PR00834; PROTEASES2C SMART; SM00228; PDZ; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     32.3%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           PROSITE; PS50106; PDZ; 1.
Hydrolase; Serine protease;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Query Match 32,39
Best Local Similarity 37,77
Matches 146; Conselvative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Nature 396:133-140(1998).
                                                                                                                                                         STANDARD;
                                                                                                                                                                                                                                                                                                                                                        prowazek11.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              513 AA,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            124
290
418
139
169
247
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  MEROPS; S01,273
                                                                                                                                                                                                                                                                                                                                                                                                                                      NCBI_TaxID=782;
                                                                                                                                                         DEGP_RICPR
                                                                                                                                                                                                                                                                                                                                                        Rickettsia
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   DOMAIN
DOMAIN
ACT_SITE
ACT_SITE
ACT_SITE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 SEQUENCE
                                                                                                                                                                                   005942;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  CHAIN
DOMAIN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     SIGNAL
                                                                                                                                                                                   q
```

122 70

셤

å

g à 셤 ö g ò g

à

LGSGVIISKDGYIVTNNHVIDGADKIKVTIPGSNKEYSATLVGTDSESDLAVIRI-TKDN

LPTIKFSDSNDISVGDLVFAIGNPFG-VGESVTQGIVSALNKSGIGI---NSYENFIQTD

186 GYLGVGLQDLSGDLQN--SYDNKEGAVVISVEKDSPAKKAGILVWDLITEVNGKKVKNTN

126 ASINPGNSGGALIDSRGGLVGINTALISKTGGNHGIGFAIPSNMVKDTVTQLIKTGKIER

244 ELRNLIGSMLPNQRVTLKVIRDKKERAFTLTLA----ERKNPNKKETISA-----QNGA 293

243

125

```
This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way
294 QGQLNGLQVEDLTQETKRSMRLSDDVQGVLVSQVNENSPAEQAGFRQGNIITKIEEVEVK 353
                                            Glazebrook J., Ichige A., Walker G.C.;
"Genetic analysis of Rhizobium meliloti bacA-phoA fusion results in identification of degP: two loci required for symbiosis are closely linked to degP.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        30-MAY-2000 (Rel. 39, Created)
30-MAY-2000 (Rel. 39, Last sequence update)
15-JUN-2002 (Rel. 41, Last annotation update)
Probable serine protease do-like precursor (EC 3.4.21.-).
DEGPI OR DEGP OR R01021 OR SMC02365.
Rhizoblam melliloti (Sinorhizobium melliloti (Sinorhizobium mellioti).
Rhizoblaceae; Sinorhizobium; alpha subdivision; Rhizoblaceae group;
                                                                                                                                                                                                                                                                                                                                                                                                 504 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         use by non-profit institutions as long a modified and this statement is not removed.
                                                                                                                                            354 SVADFNHALEKYKGKPKRFLVLDLNQG 380
                                                                                                                                                                                         : : | | | : : | : : | 476 DIRKLEVLYENAKKLEKQNILLLIERG 502
                                                                                                                                                                                                                                                                                                                                                                                                 PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         STRAIN=1021;
MEDLINE-21396507; PubMed=11481430;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         STRAIN-1021;
MEDLINE-96146524; PubMed-8550509;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        J. Bacteriol. 178:745-752(1996).
                                                                                                                                                                                                                                                                                                                                                                                             STANDARD;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 NCBI_TaxID=382;
                                                                                                                                                                                                                                                                                                                                                                                     DEGP_RHIME
Q52894;
                                                                                                                                                                                                                                                                                                                       RESULT 13
                                                                                                                                                                                                               g
                                                                      셤
                                                                                                                                                                                                                                                                                                                                                                                             HER REPARENTED TO THE SERVICE OF THE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           CCCCCCCRRRBBBBBB
ò
```

Usage by

```
entities requires a license agreement (See http://www.1sb-s1b.ch/announce/
                                                                                                                                                                                                                                                                                                                                                                                      KTVISSPTTTSSPTART (IN REF. 1).
KSADDVLKVINNAKKDGRSKALFQIEAQEGSRFVALPITQG
                                                                                                                                                                                                                                                                                                                                                                          VSSANSLRVKMTVPIVGATAAVRVAKVVSVRGRKAPASSSP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           128 INPGNSGALIDSRGGLVGINTAIISKTGGNHGIGFAIPSNMVKDTVTQLIKTGKIERGY 187
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 359 ARRVAALRPGSTAEVTLWRSGKSETVNLEIGTLPS-DAKEPAPATGEAQPD-EGQAGEEA 416
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         306 TQETKRSMRLSDDVQGVLVSQVNENSPAEQAGFRQGNIITKIEEVEVKSVAD----FNHA 361
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               417 LADLGLIVIPSEDGKGVIIASVDPDSDAGDRGLKEGEKIVSVNNQEVKSADDVLKVINNA 476
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           68 DNLPTIKFSDSNDISVGDLVFAIGNPFGVGESVTQGIVSALNKSGIGINSYENFIQTDAS 127
                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             9 RALGSGVIISKDGYIVTNNHVIDGADKIKVTIPGSNKEYSATLVGTDSESDLAVIRI-TK 67
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         246 RNLIGSMLPNORVTLKVIRDKKERAFTLTLAERKNPNKKETISAONGAOGOLNGLOVEDL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         188 LGVGLQDLSGDLQNSYDNKE--GAVVISVEKDSPAKKAGILVWDLITEVNGKKVKNTNEL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                      13;
                                                                                                                                                                                                                   POTENTIAL.
PROBABLE SERINE PROTEASE DO-LIKE.
                                                                                                                                                                                                                                                                                                                                                                                                                                             Length 504;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Indels
                                                                                                                                                                                           Periplasmic; Repeat; Signal;
                                                                                                                                                                                                                                                                                                                                                                                                             NRQTTFSR (IN REF. 1).
D7E82BB9981EA23C CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                            31.9%; Score 618.5; DB 1;
llarity 37.3%; Pred. No. 2.2e-29;
Conservative 71; Mismatches 156;
                                                                                                                                                                                                                                          CATALYTIC.
          send an email to license@isb-sib.ch)
                                                       MEROPS; S01.273;
InterPro; IPR001478;
InterPro; IPR001478;
InterPro; IPR00126; Ser_proteas_V8.
InterPro; IPR001254; Ser_protease_Try.
Pfam; PF00089; trypsin; 1.
                                 EMBL; U31512; AAC43669.1; ALT_INIT.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        362 LEKYKGKPKRFLVLDLNQGYRII 384
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      --KKDGRSKALFQIEAQEGSRFV 497
                                                                                                                                         PRINTS; PR00834; PROTEASES2C.
PRINTS; PR00839; V8PROTEASE.
SMART; SM00228; PD2; 2.
PR0512; PR0512; 2.
Hydrolase; Serine protease; Per
                                                                                                                                                                                                                                                                                                                                                                                                                       504 AA; 53035 MW;
                                             AL591785; CAC45593.1;
                                                                                                                                                                                                                   504
                                                                                                                                                                                                                                                                                                                                                                                                                                                           Local Similarity
                                                                                                                                                                                                                                          1113
287
401
140
170
244
                                                                                                                                                                                                                                                                                                                                                                                                 464
                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Matches 143;
                                                                                                                                                                                                                                                                DOMAIN
ACT_SITE
ACT_SITE
                                                                                                                                                                                                                                                                                                   ACT_SITE
CONFLICT
CONFLICT
                                                                                                                                                                                                                                                                                                                                                                                                                        SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                 CONFLICT
                                                                                                                                                                                                                                                                                                                                                                                                                                                Query Match
                                                                                                                                                                                                                                          DOMAIN
                                                                                                                                                                                                                   SIGNAL
                                                                                                                                                                                                                                 CHAIN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             477
g
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   a
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  g
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 合
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ò
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           à
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ò
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 a
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ò
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ò
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                셤
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ò
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          and for commercial
```

```
CHARGE RELAY SYSTEM (POTENTIAL).
CHARGE RELAY SYSTEM (POTENTIAL).
CHARGE RELAY SYSTEM (POTENTIAL).
LL -> PV (IN REF. 1).
PSFANVVDAVSPAVVSVRVQARERVSDDESNFTFDFGGRGF
                                                                                                          EDLPEDHPLRRFFREFAPRENDRADBMRDRROPRGEGRLRP
RAGGSGFFITEDGYLVTNNHVVSDGSA -> AVSPMMSTPF
RRRSSPSACRHVNASATMKATSPSISAAAGSRTCRKTIRCG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     503 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     STANDARD;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  DEGP_BARHE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      RESULT 14
DEGP_BARHE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     C
```

ä

```
This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EWBL outstation the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial
                                                                                                                                                                                                                                                                                                                                                                                                                            entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               æ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              68 DNLPTIKFSDSNDISVGDLVFAIGNPFGVGESVTQGIVSALNKSGIGINSYENFIQTDAS 127
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              242 VNRGNSGEPTFDLNGKVVGVNTAIFSPSGGNVGIAFAIPAATANEVVQQLIEKGLVQRGW 301
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       LGVGLQDLSGDLQNSYDNKE--GAVVISVEKDSPAKRAGILVWDLITEVNGKKVKNTNEL 245
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Anderson B., Sims K., Regnery R., Robinson L., Schmidt M.J., Goral S., Hager C., Edwards K.;
Goral S., Hager C., Edwards K.;
"Detection of Rochlimaea henselae DNA in specimens from cat scratch disease patients by PCR.";
J. Clin. Microbiol. 32:942-948(1994).
--- SUBCELLULAR LOCATION: Periplasmic (Potential).
--- SIMILARITY: BELONGS TO PEPTIDASE FAMILY $2C.
--- SIMILARITY: CONTAINS 2 PDZ/DHR DOMAINS.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          128 INPGNSGGALIDSRGGLVGINTAIISKTGGNHGIGFAIPSNMVKDTVTQLIKTGKIERGY 187
           01-OCT-1996 (Rel. 34, Created)
01-OCT-1996 (Rel. 34, Last sequence update)
15-UNN-2002 (Rel. 41, Last annotation update)
Probable periphasmic serine protease DO-like precursor (EC 3.4.21.-)
(Antigen htrA).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     PROBABLE PERIPLASMIC SERINE PROTEASE DO-
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             10 ALGSGVIISKDGYIVTNNHVI-DGADKIKVTIPGSNKEYSATLVGTDSESDLAVIRIT-K 67
                                                                                                                          Bacteria; Proteobacteria; alpha subdivision; Rhizobiaceae group;
Bartonellaceae; Bartonella.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              21;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                PDZ 2.
CHARGE RELAY SYSTEM (POTENTIAL).
CHARGE RELAY SYSTEM (POTENTIAL).
CHARGE RELAY SYSTEM (POTENTIAL).
; 6CD9F4743282AF9E CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              DB 1; Length 503;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Periplasmic; Repeat; Signal.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               39.1%; Pred. No. 2.9e-29; ive 63; Mismatches 145;
                                                                                                           Bartonella henselae (Rochalimaea henselae).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  31.8%; Score 616.5;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       POTENTIAL.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       InterPro; IPR001478; PDZ.
InterPro; IPR001940; Protease2C.
InterPro; IPR001254; Ser_protease_Try.
Pfam; PF00089; trypsin; 1.
Pfam; PF00595; PDZ; 2.
                                                                                                                                                                                                     STRAIN=Houston-1;
MEDLINE=94299828; PubMed=8027347;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  54114 MW;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      PRINTS; PR00834; PROTEASES2C.
SMART; SM00228; PDZ; 2.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              EMBL; L20127; AAA97430.1; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Serine protease;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Best Local Similarity 39.1 Matches 147; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       PS50106; PDZ;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   357
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                173
247
503 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Similarity
                                                                                                                                                                                        SEQUENCE FROM N.A.
                                                                                                                                                         NCBI_TaxID=38323;
                                                                                            DEGP OR HTRA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Hydrolase;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ACT_SITE
ACT_SITE
ACT_SITE
SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      PROSITE;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   DOMAIN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     SIGNAL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    DOMAIN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     CHAIN
g
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        셤
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ð
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ដ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                q
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ò
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ò
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ò
```

```
This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation-the Buropean Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                "Whole-genome random sequencing and assembly of Haemophilus influenzae
                                                                                                       306 IQETKRSMRL----SDDVQGVLVSQVNENSPAEQAGFRQGNIITKIEEVEVKSVADFNHA 361
                                                                                                                                   246 RNLIGSMLPNQRVTLKVIRDKKERAFTLTLAERKNPNKKETISAQNGAQGQLNGLQVEDL 305
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       MEDIANE STATE STAT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Periplasmic; Signal; Complete proteome.
                                    361 AKRIANMSPGETVTLGVWKSGKEENIKVKLDSMPEDENMKDGSKYSNEHGN----
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Bacteria; Proteobacteria; gamma subdivision; Pasteurellaceae;
Haemophilus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        (POTENTIAL)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            CHARGE RELAY SYSTEM (POTEN
CHARGE RELAY SYSTEM (POTEN
CHARGE RELAY SYSTEM (POTEN
69EA452DF5A10649 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Science 269:496-512(1995).
-!- SUBCELLULAR LACATION: Periplasmic (Potential).
-!- SIMILARITY: BELONGS TO PEPTIDASE FAMILY S2C.
-!- SIMILARITY: CONTAINS 1 PDZ/DHR DOMAIN.
                                                                                                                                                                                                                                                                                                                                                                                                                                                          01-NOV-1995 (Rel. 32, Created)
01-NOV-1995 (Rel. 32, Last sequence update)
15-JUN-2002 (Rel. 41, Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                          340 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 POTENTIAL.
PROTEASE DEGS.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Protease degS precursor (EC 3.4.21.-).
DEGS OR HHOB OR HTRH OR HI0945.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     InterPro; IPR001478; PDZ.
InterPro; IPR001940; Protease2C.
InterPro; IPR001254; Ser_protease_Try.
Pfam; PF00089; trypsin; 1.
Pfam; PF00595; PD[3; 1.
                                                                                                                                                                                                                                                                                                                                                                                                          PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             36039 MW;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    PRINTS; PR00834; PROTEASES2C.
SMART; SM00228; PDZ; 1.
PROSITE; PS50106; PDZ; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               EMBL; U32775; AAC:2599.1; -. MEROPS; S01.275; ".
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Hydrolase; Serine protease; SIGNAL 1 22
                                                                                                                                                                                                                                                      472 IKNAQKLGRKAILLQV 487
                                                                                                                                                                                                                 362 LEKYKGKPKRFLVUDL 377
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            PS50106; PDZ; 1.
                                                                                                                                                                                                                                                                                                                                                                                                          STANDARD;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Haemophilus influenzae
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           340 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          23
251
92
122
197
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 NCBI_TaxID=727;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 MEROPS; S01.27
TIGR; HI0945;
                                                                                                                                                                                                                                                                                                                                                                                                       DEGS_HAEIN
P44947;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   DOMAIN
ACT_SITE
ACT_SITE
ACT_SITE
ACT_SITE
SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          CHAIN
                                                                                                                                                                                                                                                                                                                                                                                 DEGS_HAEIN
                                                                                                                                                                                                                                                                                                                                                     RESULT 15
                                                                                                                                                                                                                                                                    셤
                                                                                                                                                                                                                                                                                                                                                                                                                                      g
                                                                                                       ά
                                                                                                                                                         q
                                                                                                                                                                                                                 ŏ
```

Search completed: November 18, 2002, 11:28:57 Job time : 16 secs

```
GenCore version 5.1.3
Copyright (c) 1993 - 2002 Compugen Ltd.
```

OM protein - protein search, using sw model

November 18, 2002, 11:28:01; Search time 22 Seconds (without alignments) 1691.092 Million cell updates/sec Run on:

US-09-895-913A-120 1938 Title: Perfect score: Sequence:

1 MIPKERMERALGSGVIISKD.......KPKRFLVLDLNQGYRIILVK 387

BLOSUM62 Gapop 10.0 , Gapext 0.5 coring table:

283224 seqs, 96134422 residues

Searched:

283224 Total number of hits satisfying chosen parameters:

Minimum DB seq length: 0 Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database:

PIR_73:*
1: pir1:*
2: pir2:*
3: pir3:*
4: pir4:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

		d			SUMMARIES	
Result No.	ပ္ပ	Query Match	ngth	DB	ID	Description
)1	1938	100.0	443	: -	C64647	serine proteinase
7	1914	98.8	476	7	H71936	
m	937	48.3	472	7	F81329	serine proteinase
4	767	6	456	7	F82307	proteinase DO VC05
5	749.5	38.7	497	7	H71465	probable do serine
9	746.5	8	497	7	B81728	serine proteinase,
7	722.5	37.3	474	7	845229	proteinase DO (EC
80			474	7	E85500	8
6	722.5		474	7	E90649	proteinase DO (EC
10	722.5	37.3	488	7	н86612	DO serine proteina
11	722.5	37.3	488	7	G81528	serine proteinase,
12	722.5	37.3	488	~	G72011	do serine proteina
13	717.5	37.0		7	AC0528	protease DO precur
14	714.5	36.9		Н	S15337	heat shock protein
15	710	36.6	453	Н	B70426	periplasmic serine
16	707.5	36.5		7	AI3349	proteinase DO (EC
17	706.5	36.5		~	F83550	serine proteinase
18	703.5	36.3		П	I40059	htrA-like protein
19	869	36.0		N	AG0433	proteinase (EC 3.4
20	692.5	35.7		7	A97479	probable serine pr
21	692.5	35.7		7	AI2696	serine proteinase
22	ď.	35.1		7	I40060	serine proteinase
23	679.5	35.1		~	AD3418	proteinase DO (EC
24	619	35.0		Н	A64113	heat shock protein
25		35.0		~	G84956	ase
26		34.4		7	AH0410	Ø
27	663.5	34.2	511	~	F97720	periplasmic serine
28	S	33.8		~	AB0909	serine protease (E
29	653	33.7	514	7	A82581	periplasmic protei

361 ALEKYKGKPKRFLVLDLNQGYRIILVK 387

QY Db δ

trypsin-like prote serine endoprotein	serine endoprotein	probable serine pr	serine proteinase	serine proteinase	htrA protein homol	heat shock protein	probable periplasm	AlgW protein PA444	serine proteinase	probable periplasm	proteinase do (EC	trypsin-like prote	periplasmic serine	serine proteinase
JC6051 C91142	F85987	C97605	AE2827	AI2811	B97590	D82826	B71722	B83089	F87590	B81914	AG3328	164103	F72359	C87408
44	7	7	7	~	N	7	N	~	~	~	7	Н	~	7
455 455	455	493	514	468	495	481	513	389	530	499	524	340	459	472
10.10	9	و	७.	0	0.	∞.	۳.		0	σ.	~	بو	0.	ω.
33.6	33.	33	33	33	33	32	32	32	31	30	30	28	28	27
652 33.6 652 33.6	651.5 33.	651 33.	651 33	639 33					601.5 31				542.5 28	

ALIGNMENTS

RESULT 1

-	1 110000	
	CO404/ Control note insect (DC 3 / 21 -) - Holidobactor mylori (strain 26605)	otrain 266051
_		Sciain 20033)
	C.Date: 10-Sep-1999 #skiquence_revision 10-Sep-1999 #text_change 09-Jun-2000	t_change 09-Jun-2000
	C; Accession: C64647	
	R; Tomb, J.F.; White, O.; Kerlavage, A.R.; Clayton, R.A	; Sutton, G.G.; Fleischmann, R
	Peterson, S.; Lottus, B.; Richardson, D.; Dodson, R.;	Khalak, H.G.; Glodek, A.; McKe
	Son, J.D.; Kelley, J.M.; Cotton, M.D.; Weldman, J.M.; Fujll, C.; Bowman, C.; Watthey, Nature 388 530-547 1007	'ujii, C.; Bowman, C.; Watthey,
-	A; Authors: Wallin, E.; Haves, W.S.; Borodovsky, M.; Karpk, P.D.; Smith, H.O.; Fraser,	pk, P.D.; Smith, H.O.; Fraser,
	A; Title: The complete genome sequence of the gastric pathogen Helicobacter pylori.	thogen Helicobacter pylori.
	A; Reference number: A64520; MUID:97394467; PMID:9252185	
	A:Status: preliminary; nucleic acid sequence not shown; translation not	translation not shown
	A, Molecule type: DNA	
_	A; Residues: 1-443 <10M.>	160. gram. handoogs 1. gram. 2331
	ACTIONS-TELEGERICES: GB:AECUCOLU; GB:AECUCOLL; NID:GZ314100; FIDN:AADUGUG3.1; FID:GZ31	TOO! FIDN: AADUGUGS: 1; FID: 9231
-	A:Start andon: GTS	
-	C; Superfamily: Helicobacter serine proteinase	
-	C; Keywords: hydrolase; serine proteinase	
	100.08;	Length 443;
	Best Local Similarity 100.0%; Pred. No. 2.9e-111; Matches 387; Conservative 0; Mismatches 0;	Indels 0; Gaps 0;
	QY 1 MIPKERMERALGSGVIISKDGYIVTNNHVIDGADKIKVTIPGSNKEYSATLVGTDSESDL	EYSATLVGTDSESDL 60
	Db 57 MIPKERMERALGSGVIISKDGYIVTNNHVIDGADKIKVTIPGSNKEYSATLVGTDSESDL 116	
	; ;	
	Qy 61 AVIRITKBNLPT!TKFSDSNDISVGDLVFAIGNPFGVGESVTQGIVSALNKSGIGINSYEN	/SALNKSGIGINSYEN 120
	Db 117 AVIRITKDNLPTIKFSDSNDISVGDLVFAIGNPFGVGESVTQGIVSALNKSGIGINSYEN	SALNKSGIGINSYEN 176
	Qy 121 FIQTDASINPGNSGGALIDSRGGLVGINTALISKTGGNHGIGFAIPSNMVKDTVTQLIKT	PSNMVKDTVTQLIKT 180
	Db 177 FIQTDASINPGN/SGGALIDSRGGLVGINTAIISKTGGNHGIGFAIPSNMVKDTVTQLIKT	PSNMVKDTVTQLIKT 236
	QY 181 GKIERGYLGVGL)DLSGDLQNSYDNKEGAVVISVEKDSPAKKAGILVWDLITEVNGKKVK	LVWDLITEVNGKKVK 240
	Db 237 GKIERGYLGVGLJDLSGDLQNSYDNKEGAVVISVEKDSPAKKAGILVWDLITEVNGKKVK	LINDLITEVNGKKVK 296
	QY 241 NTNELRNLIGSMUPNORVTLKVIRDKKERAFTLTLAERKNPNKKETISAONGAOGOLNGL	TISAQNGAQGQLNGL 300
	Db 297 NTNELRNLIGSM", PNQRVTLKVIRDKKERAFTLTLAERKNPNKKETISAQNGAQGQLNGL	TISAQNGAQGQLNGL 356
-		

ů,

161

249

Nov

```
A; Residues: 1-472 <PAR>
A; Residues: 1-472 <PAR>
A; Cross-references: GB:AL139077; GB:AL111168; NID:g6968444; PIDN:CAB73482.1; PID:g696
A; Experimental source: serotype O2, strain NCTC 11168
C; Genetics:
A; Genetics:
C; Superfamily: Helicobacter serine proteinase
C; Superfamily: Helicobacter serine proteinase
C; Reywords: hydrolase; serine proteinase
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        PIDN: AAF93734.1; GSPDB:GN
El Tor
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Gwinn, M.L.; Dodson, R.
H.; Dragoi, I.; Sellers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          proteinase DO VC0566 [imported] - Vibrio cholerae (strain N16961 serogroup 01) C; Species: Vibrio cholerae (c;Date: 18-Aug-2000 #sequence_revision 20-Aug-2000 #text_change 02-Feb-2001 C; Accession: F82307 Feb-2001 R; Heidelberg, J.F.; Eisen, J.A.; Nelson, W.C.; Clayton, R.A.; Gwinn, M.L.; Dodson, Chardson, D.; Ermolaeva, M.D.; Vamathevan, J.; Bass, S.; Qin, H.; Dragoi, I.; Sell I. R.R.; Mekalanos, J.J.; Venter, J.C.; Fraser, C.M. Nature 406, 477-483, 2000 A; Title: DNA Sequence of both chromosomes of the cholera pathogen Vibrio cholerae. A; Reference number: A82035; MUID: 204006833; PMID: 10952301
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             250 GSMLPNQRVTLKVIRD--KKERAFTLTLAERKNPNKKETISAQNGAQGQL-NGLQVEDLT 306
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           70 LPTIKFSDSNDISVGDLVFAIGNPFGVGESVTQGIVSALNKSGIGINSYENFIQTDASIN 129
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             130 PGNSGGALIDSRGGLVGINTAIISKTGGNHGIGFAIPSNMVKDTVTQLIKTGKIERGYLG 189
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   307 QETKRSMRLSDDVQGVLVSQVNENSPAEQAGFRQGNIITKIEEVEVKSVADFNHALEKYK 366
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             63 IRITK-DNLPTIKFSDSNDISVGDLVFAIGNPFGVGESVTQGIVSALNKSGIGINSYENF 121
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 4 KERMERALGSGVIISKD-GYIVTNNHVIDGADKIKVTIPGSNKEYSATLVGTDSESDLAV 62
                                                                                                                                                                                                                                                                                                                                                                                                                                                                     162 LSAITFTNSDDLMEGDVVFALGNPFGVGFSVTSGIISALNKDNIGLNQYENFIQTDASIN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     10 ALGSGVIISKDGYIVTNNHVIDGADKIKVTIPGSNKEYSATLVGTDSESDLAVIRITKDN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      190 VGLQDLSGDLQNSYDNKEGAVVISVEKDSPAKKAGILVWDLITEVNGKKVKNTNELRNLI
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    14;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                22;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Length 456;
                                                                                                                                                                                                                                                                                                                                                    Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           39.6%; Score 767; DB 2; Length 45 ilarity 43.6%; Pred. No. 1.3e-39; Conservative 83; Mismatches 112; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               GB:AE003852; NID:99654988;
O1; strain N16961; biotype
                                                                                                                                                                                                                                                                               ; Score 937; DB 2; L
; Pred. No. 5.5e-50;
69; Mismatches 102;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              A; Status: preliminary
A; Status: preliminary
A; Molecule type: DNA
A; Residuas: 1-456 < HEI>
A; Experimental source: serogroup Ol; strain N1699
C; Genetics:
A; Genetics:
A; Genetics:
C; 
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            GKPKRFLVLDLNQGYRIILV 386
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              451 NKKEFTKVWVYRNGFATLLV 470
                                                                                                                                                                                                                                                                                   Query Match
Best Local Similarity 51.3%;
Matches 195; Conservative 65
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Query Match
Best Local Similarity
Matches 168; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            367
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       RESULT 4
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          g
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       à
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        g
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          QQ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ò
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           g
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          qq
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        QQ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              g
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      g
                                                                                                                                                                                                                                                                                                                                                                                                                                    à
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             à
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ŏ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ò
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               δλ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ð
                                                                                                                                                                                                       proteinase Do - Helicobacter pylori (strain J99)
C;Species: Helicobacter pylori
A;Variety: Strain J99
C;Species: Helicobacter pylori
A;Vatriety: Strain J99
C;Date: 12-Feb-1999 #sequence_revision 12-Feb-1999 #text_change 20-Sep-1999
C;Accession: H71336
R;Alm, R.A.; Ling, L.S.L.; Moir, D.T.; King, B.L.; Brown, E.D.; Doig, P.C.; Smith, D.R.; Ives, C.; Gibson, R.; Merberg, D.; Mills, S.D.; Jiang, Q.; Taylor, D.E.; Vovis, G.F.; Nature 397, 176-180, 1999
Nature 397, 176-180, 1999
A;Title: Genomic sequence comparison of two unrelated isolates of the human gastric path A;Reference number: A71800; MUID:99120557; PMID:9923682
A;Accession: H71936
A;Accession: H71936
A;Status: preliminary
A;Aolecule type: DNA
A;Residues: 1-476 <ARN>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      RESULT 3
F81329
Serine proteinase (proteinase DO) (EC 3.4.21.-) Cj1228c [imported] - Campylobacter jejun
C;Species: Campylobacter jejuni
C;Date: 31-Mar-2000 #sequence_revision 31-Mar-2000 #text_change 03-Jun-2002
C;Date: 31-Mar-2000 #sequence_revision 31-Mar-2000 #text_change 03-Jun-2002
C;Accession: F81329
R;Parkhill, J.; Wren, B.W.; Mungall, K.; Ketley, J.M.; Churcher, C.; Basham, D.; Chillin
C.W.; Quail, M.; Rajandream, M.A.; Rutherford, K.M.; VanVilet, A.; Whitehead, S.; Barrel
Nature 403, 665-668, 2000
A;Title: The genome sequence of the food-borne pathogen Campylobacter jejuni reveals hyg
A;Reference number: A81250; WUID:20150912; PMID:10688204
A;Accession: F81329
A;Status: preliminary
A:Wolecule type: DNA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                GB:AE001439; NID:g4154929; PIDN:AAD05980.1; PID:g415493
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               210 FIQTDASINPGNSGGALIDSRGGLVGINTAIISKTGGNHGIGFAIPSNMVKDIVTQLIKT 269
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    GKIERGYLGVGLQDLSGDLQNSYDNKEGAVVISVEKDSPAKKAGILVWDLITEVNGKKVK 240
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            NTNELRNLIGSMLPNQRVTLKVIRDKKERAFTLTLAERKNPNKKETISAQNGAQGQLNGL 300
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                90 MIPKERMERALGSGVIISKDGYIVTNNHVIDGADKIKVTIPGSNKEYSATLVGTDSESDL 149
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        61 AVIRITKDNLPTIKFSDSNDISVGDLVFALGNPFGVGESVTQGIVSALNKSGIGINSYEN 120
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          121 FIQTDASINPGNSGALIDSRGGLVGINTAIISKTGGNHGIGFAIPSNMVKDTVTQLIKT 180
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 1 MIPKERMERALGSGVIISKDGYIVTNNHVIDGADKIKVTIPGSNKEYSATLVGTDSESDL 60
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Length 476;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                4 :
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Query Match
98.8%; Score 1914; DB 2;
Best Local Similarity 98.7%; Pred. No. 9.3e-110;
Matches 382; Conservative 1; Mismatches 4;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Superfamily: Helicobacter serine proteinase
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              361 ALEKYKGKPKRFLVLDLNQGYRIILVK 387
A;Cross-references: GB:AE001474; CA;Experimental source: strain J99
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Gene: htrA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Genetics:
                                    417
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    181
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           450
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              241
                                    a
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Ω
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ò
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Q
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ò
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  셤
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    g
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           g
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ò
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   g
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ò
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ð
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ð
```

```
Serine proteinase, Htrk/Degg/Degs family TC0210 [imported] - Chlamydia muridarum (str C;Species: Chlamydia muridarum, Chlamydia trachomatis Mopn C;Date: 31-Mar-2000 #sequence_revision 31-Mar-2000 #text_change 21-Jul-2000 C;Accession: B81728 Rsead, T.D.; Bruhham, R.C.; Shen, C.; Gill, S.R.; Heidelberg, J.F.; White, O.; Hicke C.; Dodson, R.; Gwina, M.; Nelson, W.; Beboy, R.; Kolonay, J.; McClarty, G.; Salzbe Nucleic Acids Res. 28, 1397-1406, 2000 Rs; Kolonay, J.; McClarty, G.; Salzbe A;Hitle: Genome sequences of Chlamydia trachomatis Mopn and Chlamydia pneumoniae AR39 A;Accession: B81728 A;Accession: B81728 A;Atatus: preliminary A;Molecule type: DNA A;Accession: B81728 A;Accessio
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             A;Residues: 1-497 <TET>
A;Residues: 1-497 <TET>
A;Cross-references: GB:AE002160; NID:g7190247; PIDN:AAF39082.1; PID:g719
A;Cross-references: strain Nigg (MoPn)
C;Genetics: A;Gene: TC0210
C;Superfamily: Helicobacter serine northeirs
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               RESULT 7
S45229
Stoches: Escherichia coli
C; Date: 13-Jan-1995 #scquence_revision 13-Jan-1995 #text_change 01-Mar-2002
C; Date: 13-Jan-1995 #scquence_revision 13-Jan-1995 #text_change 01-Mar-2002
C; Date: 13-Jan-1995 #scquence_revision 13-Jan-1995 #text_change 01-Mar-2002
C; Accession: S45229; A64740; S01899; B35993
R; Fujita, N.
Submitted to the EMBL Nata Library, January 1994
A; Reference number: S45181
A; Accession: S4529
A; Cross-references: EMEL: D26562; NID: 9473770; PIDN: BAA05608.1; PID: 9473819
A; Cross-references: EMEL: D26562; NID: 9473770; A; Experimental source: Strain R-12, substrain W3110
B; Blattner, F.R.; Plunkett III, G.; Bloch, C.A.; Perna, N.T.; Burland, V.; Riley, M.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           7;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  240
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 IRITKDNLPTIKFSDSNDISVGDLVFAIGNPFGVGESVTQGIVSALNKSGIGINSYENFI 122
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            QTDASINPGNSG3ALIDSRGGLVGINTAIISKTGGNHGIGFAIPSNMVKDTVTQLIKTGK 182
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         LQVEDLTQETKR:3MRLSDDVQGVLVSQVNENSPAEQAGFRQGNI 1TK1EEVEVKSVADFN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     3 PKERMERALGSGYIISKDGYIVTNNHVIDGADKIKVTIPGSNKEYSATLVGTDSESDLAV
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  IERGYLGVGLQD:SGDLQNSY - - DNKEGAVVISVEKDSPAKKAGILVWDLITEVNGKKVK
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   NTNELRNLIGSMÄPNORVTLKVIRDKKERAFTLTLAERKNPNKKETISAONGAOG-QLNG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           19;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Length
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            38.5%; Score 746.5; DB 2;
41.3%; Pred. No. 2.7e-38;
iive 84; Mismatches 126;
           |: ||: ||: 468 QVLKNSKGEN---VLLMVSQGDVVRFIVLK 494
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      360 HALEKYKGKPKRIFLVLDLNQG--YRIILVK 387
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Best_Local Similarit; 41.39
Matches 161; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            123
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     300
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           63
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  183
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 468
                                               셤
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            a
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  a
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               셤
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        a
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ò
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ŏ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ò
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              à
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Q
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ð
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  g
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ŏ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ò
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         g
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            probable do serine proteinase - Chlamydia trachomatis (serotype D, strain UW3/Cx)
probable do serine proteinase - Chlamydia trachomatis
C;Species: Chlamydia trachomatis
C;Species: Chlamydia trachomatis
C;Species: 13-Sep-1998 #sequence_revision 13-Sep-1998 #text_change 08-Oct-1999
C;Accession: H71465
R;Stephens, R.S.; Kalman, S.; Lammel, C.J.; Fan, J.; Marathe, R.; Aravind, L.; Mitchell, A;Stephens, R.S.; Kalman, S.; Lammel, C.J.; Fan, J.; Marathe, R.; Aravind, L.; Mitchell, A;Title: Genome sequence of an obligate intracellular pathogen of humans: Chlamydia trach. A;Reference number: A71570; MUID:99000809; PMID:9784136
A;Status: preliminary
A;Molecule type: DNA
A;Residues: 1-497 <ARN>
A;Residues: 1-497 <ARN>
A;Residues: 1-497 <ARN>
A;Residues: 1-497 <ARN>
A;Resperimental source: serotype D, strain UW-3/Cx
C;Genetics:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       1;
                                                                                                                                                                                                                                                                                                                                              323
                                                                                                                                                                                                                                                                                                                                                                                                                             299
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   378
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              :::| ::||::|:::|
379 AELSNTTD------SDPIQGVKVTEVQKGSAAESYQLQKDDIIIGVNKKRVKNIAELR 430
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 296
                                                                                                                                                                                                                                                                   KIERGYLGVGLQDLSGDLQNS--YDNKEGAVVISVEKDSPAKKAGILVWDLITEVNGKKV 239
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      LQVEDLTQETKRSMRLSDDVQGVLVSQVNENSPAEQAGFRQGNIITKIEEVEVKSVADFN 359
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               IRITKDNLPTIKFSDSNDISVGDLVFAIGNPFGVGESVTQGIVSALNKSGIGINSYENFI 122
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      QTDASINPGNSGGALIDSRGGLVGINTAIISKTGGNHGIGFAIPSNMVKDTVTQLIKTGK 182
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      IERGYLGVGLQDLSGDLQNSY--DNKEGAVVISVEKDSPAKKAGILVWDLITEVNGKKVK 240
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             : ||:||| || : :| || : ||:|: ||:|: ||:|: ||:|: ||:|: ||:|: ||:|: ||:|: ||:|: ||:|: ||:|: ||:|: ||:|: ||:|: ||:|: ||:|: ||:|: ||:|: ||:|: ||:|: ||:|: ||:|: ||:|: ||:|: ||:|: ||:|: ||:|: ||:|: ||:|: ||:|: ||:|: ||:|: ||:|: ||:|: ||:|: ||:|: ||:|: ||:|: ||:|: ||:|: ||:|: ||:|: ||:|: ||:|: ||:|: ||:|: ||:|: ||:|: ||:|: ||:|: ||:|: ||:|: ||:|: ||:|: ||:|: ||:|: ||:|: ||:|: ||:|: ||:|: ||:|: ||:|: ||:|: ||:|: ||:|: ||:|: ||:|: ||:|: ||:|: ||:|: ||:|: ||:|: ||:|: ||:|: ||:|: ||:|: ||:|: ||:|: ||:|: ||:|: ||:|: ||:|: ||:|: ||:|: ||:|: ||:|: ||:|: ||:|: ||:|: ||:|: ||:|: ||:|: ||:|: ||:|: ||:|: ||:|: ||:|: ||:|: ||:|: ||:|: ||:|: ||:|: ||:|: ||:|: ||:|: ||:|: ||:|: ||:|: ||:|: ||:|: ||:|: ||:|: ||:|: ||:|: ||:|: ||:|: ||:|: ||:|: ||:|: ||:|: ||:|: ||:|: ||:|: ||:|: ||:|: ||:|: ||:|: ||:|: ||:|: ||:|: ||:|: ||:|: ||:|: ||:|: ||:|: ||:|: ||:|: ||:|: ||:|: ||:|: ||:|: ||:|: ||:|: ||:|: ||:|: ||:|: ||:|: ||:|: ||:|: ||:|: ||:|: ||:|: ||:|: ||:|: ||:|: ||:|: ||:|: ||:|: ||:|: ||:|: ||:|: ||:|: ||:|: ||:|: ||:|: ||:|: ||: ||:|: ||:|: ||:|: ||:|: ||:|: ||:|: ||:|: ||:|: ||:|: ||:|: ||: ||:|: ||:|: ||:|: ||:|: ||:|: ||:|: ||:|: ||:|: ||:|: ||:|: ||: ||:|: ||:|: ||:|: ||:|: ||:|: ||:|: ||:|: ||:|: ||:|: ||:|: ||: ||:|: ||:|: ||:|: ||:|: ||:|: ||:|: ||:|: ||:|: ||:|: ||:|: ||: ||:|: ||:|: ||:|: ||:|: ||:|: ||:|: ||:|: ||:|: ||:|: ||:|: ||: ||:|: ||:|: ||:|: ||:|: ||:|: ||:|: ||:|: ||:|: ||:|: ||:|: ||: ||:|: ||:|: ||:|: ||:|: ||:|: ||:|: ||:|: ||:|: ||:|: ||:|: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: 
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        NTNELRNLIGSMLPNORVTLKVIRDKKERAFTLTLAERKNPNKKETISAQNGAQG-QLNG 299
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   LQVEDLTQETKRSMRLSDDVQGVLVSQVNENSPAEQAGFRQGNIITKIEEVEVKSVADFN 359
                                                                                                                      IQTDASINPGNSGALIDSRGGLVGINTAIISKTGGNHGIGFAIPSNMVKDTVTQLIKTG 181
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Gaps
KNTNELRNLIGSMLPNQRVTLKVIRDKKERAFTLTLAERKNPNKKETISAQNGAQGQLNG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          3 PKERMERALGSGVIISKDGYIVTNNHVIDGADKIKVTIPGSNKEYSATLVGTDSESDLAV
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   19;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Length 497;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Query Match 38.7%; Score 749.5; DB 2; Best Local Similarity 41.3%; Pred. No. 1.7e-38; Matches 161; Conservative 84; Mismatches 126;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Superfamily: Helicobacter serine proteinase
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   360 HALEKYKGKPKRFLVLDLNQG--YRIILVK 387
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                HALEKYKGKPKRFLVLDLNQGYRII 384
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  431 AIME----KSPNILALNIQRGERTL 451
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Gene: htrA
                                                                                                                                                                                        204
                                                                                                                                                                                                                                                                                                                                                                                                                         240
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           324
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                119
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           63
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 123
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       237
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  183
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        241
                                                                                                                  122
                                                                                                                                                                                                                                                                   182
                                                                                                                                                                                                                                                                                                                                              264
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      300
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             297
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  357
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             300
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        408
                                       셤
                                                                                                              à
                                                                                                                                                                                 g
                                                                                                                                                                                                                                                               ò
                                                                                                                                                                                                                                                                                                                                      g
                                                                                                                                                                                                                                                                                                                                                                                                                     à
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    g
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     g
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ŏ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           g
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ద
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ò
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              g
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ò
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            g
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              δ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ò
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          g
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             g
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ò
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            g
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ò
```

us-09-895-913a-120_2.rpr

```
D.J.; May
K.; Apoda
                                                                                                                                                                                                                                                                                                                                              A;Cross-references: GB:AE005174; NID:g12512885; PIDN:AAG54465.1; GSPDB:GN00145; UWGP: A;Experimental source: strain 0157:H7, substrain EDL933
C;Genetics:
A;Gene: htra
C;Superfamily: Helicobacter serine proteinase
C;Keywords: hydrolase; serine proteinase
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  proteinase DO (EC 3.4.21.-) precursor / heat shock protein ECs0165 [imported] - Esche C; Species: Escherichia coli C; C; Deteina coli C; Decies: Escherichia coli C; Decies: Escherichia coli Esequence_revision 18-Jul-2001 #text_change 17-May-2002 C; Accession: E90649
R; Hayashi, T.; Makino, K.; Ohnishi, M.; Kurokawa, K.; Ishii, K.; Yokoyama, K.; Han, C gasawara, N.; Yasunagay, T.; Kuhara, S.; Shiba, T.; Hattori, M.; Shinagawa, H. DNA Res. 8, 11-22, 2001
A; Title: Complete genome sequence of enterohemorrhagic Escherichia coli O157:H7 and ch. Recession: E90649
A; Recession: E90649
A; Residues: Preliminary
A; Molecule type: DNA
A; Molecule type: DNA
A; Residues: 1474 < ANA
A; Cross references: GB:BA000007; PIDN:BAB33588.1; PID:g13359621; GSPDB:GN00154
A; Experimental source: strain O157:H7, substrain RIMD 0509952
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ŝ
C;Date: 16-Feb-2001 #sequence_revision 16-Feb-2001 #text_change 17-May-2002 C;Accession: E85500
B;Perna, N.T.; Plunkett III, G.; Burland, V.; Mau, B.; Glasner, J.D.; Rose, D.; Aller, L.; Grotbeck, E.J.; Davis, N.W.; Lim, A.; Dimalanta, E.; Potamousis, K., Nature 409, 529-533, 2001
A;Title: Genome sequence of enterohemorrhagic Escherichia coli O157:H7.
A;Reference number: A85480; MUID:21074935; PMID:11206551
A;Status: preliminary
A;Molecule type: DNA
A;Residues: 1-474 <STO>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                68 DNLPTIKFSDSNDISVGDLVFAIGNPFGVGESVTQGIVSALNKSGIGINSYENFIQTDAS 127
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      128 INPGNSGALIDSRGGLVGINTAIISKTGGNHGIGFAIPSNMVKDTVTQLIKTGKIERGY 187
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            246 RNLIGSMLPNQRVTLKVIRDKKERAFTLTLAERKNPNKKETISAQNGAQGQLNGLQVEDL 305
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  306 TOETKRSMRLSDDVQGVLVSQVNENSPAEQAGERQGNLITKIEEVEVKSVADENHALEKY 365
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 10 ALGSGVIISKD-GYIVTNNHVIDGADKIKVTIPGSNKEYSATLVGTDSESDLAVIRI-TK 67
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         LGVGLQDLSGDLQNS--YDNKEGAVVISVEKDSPAKKAGILVWDLITEVNGKKVKNTNEL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      25;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Length 474;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           37.3%; Score 722.5; DB 2;
43.5%; Pred. No. 7.3e-37;
11ve 74; Mismatches 113;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             C,Genetics:
A,Gene: ECs0165
C;Superfamily: Helicobacter serine proteinase
C;Keywords: hydrolase; serine proteinase
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Best Local Similarity 43.5%
Matches 163; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        366 KGKPKRFLVLDLNQG 380
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             453 -SKPS-VLALNIQRG 465
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ò
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            යි
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ద
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              g
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 g
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       g
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          qq
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ŏ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ò
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ò
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ò
                                                                                                                                                                                                   A; Residues: 1-474 < CBLAT>
A; Cross references: GB:AE000125; GB:U00096; NID:g1786348; PIDN:AAC73272.1; PID:g1786356;
A; Experimental source: strain K-12, substrain MG1655
A; Experimental source: strain K-12, substrain MG1655
R; Liphinska, B.; Gargopoulos, C.
Nucleic Acids Res. 16, 10053-10067, 1988
A; Title: Sequence analysis and regulation of the htrA gene of Escherichia coli: a sigma(A; Reference number: S01899; MUD:89057448; PMID:3057437
A; Recession: S01899
A; Molecule type: DNA
A; Residues: 1-9, 'R', 11-191, 'G', 193-466,' RHLPVNAVISLNPFLKTGRGSPYNL' < LIP>
A; Residues: 1-9, 'R', 11-191, 'G', 193-466,' RHLPVNAVISLNPFLKTGRGSPYNL' < LIP>
A; Residues: 1-9, 'R', 11-191, 'G', 193-466,' RHLPVNAVISLNPFLKTGRGSPYNL' < LIP>
A; Residues: 1-9, 'R', 11-191, 'G', 193-466,' RHLPVNAVISLNPFLKTGRGSPYNL' < LIP>
A; Reperimental source: strain K-12
B; Wurgler, S.M.; Richardson, C.C.
Proc. Natl. Acad. Sci. U.S.A. 87, 2740-2744, 1990
A; Title: Structure and regulation of the gene for dGTP triphosphohydrolase from Escheric A; Reference number: A35993; MUID:90207273; PMID:2157212
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 proteinase DO (EC 3.4.21.-) precursor / heat shock protein htrA - Escherichia coli (stra
C;Species: Escherichia coli
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            9
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                188 LGVGLQDLSGDLQNS--YDNKEGAVVISVEKDSPAKKAGILVWDLITEVNGKKVKNTNEL 245
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         128 INPGNSGGALIDSRGGLVGINTAIISKTGGNHGIGFAIPSNMVKDTVTQLIKTGKIERGY 187
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  246 RNLIGSMLPNQRVTLKVIRDKKERAFTLTLAERKNPNKKETISAQNGAQGQLNGLQVEDL 305
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     306 TQETKRSMRLSDDVQGVLVSQVNENSPAEQAGFRQGNIITKIEEVEVKSVADFNHALEKY 365
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       10 ALGSGVIISKD-GYIVTNNHVIDGADKIKVTIPGSNKEYSATLVGTDSESDLAVIRI-TK 67
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Status: preliminary
Molecule type: DNA
F. Residues: 1-9, K', 11-16 <WUR>
A; Cross-references: GB:M31772; NID:g145733; PIDN:AAA23680.1; PID:g145736
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       | :|:| ::|| |:|| 351 RAQVGTMPVGSKLTLGLLRDGKQVNVNLEL-QQSSQNQVDSSSIFNGIEG------
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         25;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 DB 2; Length 474;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     C; Keywords: hydrolase; serine proteinase
F;1-26/Domain: signal sequence #status predicted <SIG>
F;27-474/Product: heat shock protein htrA #status predicted <MAT>
                                                                                                                               A; Accession: A64740
A; Status: nucleic acid sequence not shown; translation not shown
A; Molecule type: DNA
                                                                          Escherichia col1 K-12.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Query Match 37.3%; Score 722.5; DB 2; Length Best Local Similarity 43.5%; Pred. No. 7.3e-37; Matches 163; Conservative 74; Mismatches 113; Indels
                                                                       A; Title: The complete genome sequence of Escherichia co. A; Reference number: A64720; MUID:97426617; PMID:9278503
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  C; Superfamily: Helicobacter serine proteinase
         .A.; Rose, D.J.; Mau, B.; Shao, Y. Science 277, 1453-1462, 1997
A;Title: The complete genome sequen
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             KGKPKRFLVLDLNQG 380
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  -SKPS-VLALNIORG 465
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    A;Gene: htrA
A;Map position: 4 min
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            C;Genetics:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            RESULT 8
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     g
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              g
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          g
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         q
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ð
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ò
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    g
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ò
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ò
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          õ
```

U

Esche

294

```
C;Accession: G8158
R;Read, T.D.; Brunham, R.C.; Shen, C.; Gill, S.R.; Heidelberg, J.F.; White, O.; Hicke R; Read, T.D.; Brunham, R.C.; Shen, C.; Gill, S.R.; Heidelberg, J.F.; White, O.; Hicke C.; Godson, R.; Gwinn, M.; Nelson, W.; DeBoy, R.; Kolonay, J.; McClarty, G.; Salzbe Nucleic Acids Res. 28, 1397-1406, 2000
A;Title: Genome sequences of Chlamydia trachomatis MoPn and Chlamydia pneumoniae AR39 A;Reference number: A81500; MUID:20150255; PMID:10684935
A;Status: preliminary
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                A;Cross-references: GB:AE002246; GB:AE002161; NID:g7189785; PIDN:AAF38665.1; PID:g718
A;Experimental source: strain AR39, HL cells
C;Genetics:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                         serine proteinase, HtrN/DegQ/DegS family CP0877 [imported] - Chlamydophila pneumoniae C;Species: Chlamydophila pneumoniae, C;Species: 31-Mar_2000 #sequence_revision 31-Mar-2000 #text_change 21-Jul-2000
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          G72011
do serine proteinase - Chlamydophila pneumoniae (strain CWL029)
C;Species: Chlamydophila pneumoniae, Chlamydia pneumoniae
C;Date: 23-Apr-1999 #sequence_revision 23-Apr-1999 #text_change 05-May-2000
C;Accession: G72011
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    117 SYENFIQTDASINPGNSGGALIDSRGGLVGINTAIISKTGGNHGIGFAIPSNMVKDTVTQ 176
                                                                                                                                                              -QRVGIRVQNLTPETAKKLGIAPETKGILIISVEPGSVAASSGIAPGQLILAVNRQKVSS 453
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ESDLAVIRITKDNLPTIKFSDSNDISVGDLVFAIGNPFGVGESVTQGIVSALNKSGIGIN 116
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  -QRVGIRVQNLTFETAKKLGIAPETKGILIISVEPGSVAASSGIAPGQLILAVNRQKVSS
      NGKKVKNTNELRI1LIGSMLPNQRVTLKVIRDKKERAFTLTLAERKNPNKKETISAQNGAQ
                                                                                                                              GOLNGLOVEDLT()ETKRSMRLSDDVQGVLVSQVNENSPAEQAGFROGNIITKIEEVEVKS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     2 IPKER-----MERALGSGVIISKDGYIVTNNHVIDGADKIKVTIPGSNKEYSATLVGTDS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            177 LIKTGKIERGYLGVGLQDLSGDLQNSY--DNKEGAVVISVEKDSPAKKAGILVWDLITEV
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ||: ||: ||:||| || : :| | : ||:| || ||| ||| ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        NGKKVKNTNELRA)LIGSMLPNQRVTLKVIRDKKERAFTLTLAERKNPNKKETISAQNGAQ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               295 GQLNGLQVEDLTGETKRSMRLSDDVQGVLVSQVNENSPAEQAGFRQGNIITKIEEVEVKS
                                                          342 NGKEVDSLSMFRIJAVSLMNPDTRIVLKVVREGKVIEIPVTVSQAP---KEDGMSAL----
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Length 488;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      37.3%; Score 722.5; DB 2;
40.0%; Pred. No. 7.7e-37;
ive 82; Mismatches 134;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           : | | | | ::| ::| | ::| IEDLNRTL---KPSNNENILLMVSQGDVIRFIALK 485
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           VADFNHALEKYKGKPKRFLVLDLNQG--YRIILVK 387
                                                                                                                                                                                                                                                      355 VADFNHALEKYKGKPKRFLVLDLNQG--YRIILVK
                                                                                                                                                                                                                                                                                             : | | | :: | :: | | :: | IEDLNRTL---KI)SNNENILLMVSQGDVIRFIALK
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               A;Gene: CP0877
C;Superfamily: Helicobacter serine proteinase
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Query Match 37.3%
Best Local Similarity 40.0%
Matches 158; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      A; Molecule type: DNA A; Residues: 1-488 <REA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           CP0877
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        235 1
                                                                                                                                                                                                                                                                                                                                                                                                                 RESULT 11
G81528
      235
                                                                                                                              295
                                                                                                                                                                                                                                                                                                                   454
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             27
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             395
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  454
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                RESULT 12
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            g
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                g
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   q
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          g
                                                                g
                                                                                                                                                                                        ద
                                                                                                                                                                                                                                                   ò
                                                                                                                                                                                                                                                                                                                g
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ò
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ò
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               셤
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ò
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ŏ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               g
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ŏ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ò
                                                                                                                              ð
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ò
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               RESULT 10
H86612
C) Serine proteinase [imported] - Chlamydophila pneumoniae (strain J138)
C) Serine proteinase [imported] - Chlamydophila pneumoniae
C) Species: Chlamydophila pneumoniae, Chlamydia pneumoniae
C) Secies: Chart-2001 #sequence_revision 02-Mar-2001 #text_change 23-Mar-2001
C) Seciesion: H86612
Nucleic Acids Res. 28, 2311-2314, 2000
Mycleic Research and Research R86491: MUDD: 20330349; PMID: 10871362
SAccession: H86612
                                                                6
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     7;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              A;Cross-references: GB:BA000008; NID:g8979352; PIDN:BAA99186.1; GSPDB:GN00142 A;Experimental source: strain J138 C;Genetics: A;Genetics: htra A;Genetics: htra C;Superfamily: Helicohemics
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ESDLAVIRITKDNLPTIKFSDSNDISVGDLVFAIGNPFGVGESVTQGIVSALNKSGIGIN 116
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  SYENFIQTDASINPGNSGGALIDSRGGLVGINTAIISKTGGNHGIGFAIPSNMVKDTVTQ 176
                                                                                                                                                           128 INPGNSGGALIDSRGGLVGINTAIISKTGGNHGIGFAIPSNMVKDTVTQLIKTGKIERGY 187
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         LGVGLQDLSGDLQNS--YDNKEGAVVISVEKDSPAKKAGILVWDLITEVNGKKVKNTNEL 245
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 RNLIGSMLPNQRVTLKVIRDKKERAFTLTLAERKNPNKKETISAQNGAQGQLNGLQVEDL 305
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           DNLPTIKFSDSNDISVGDLVFAIGNPFGVGESVTQGIVSALNKSGIGINSYENFIQTDAS 127
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   LIKTGKIERGYLGVGLQDLSGDLQNSY - - DNKEGAVVISVEKDSPAKKAGILVWDLITEV 234
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               2 IPKER-----MERALGSGVIISKDGYIVTNNHVIDGADKIKVTIPGSNKEYSATLVGTDS 56
                                                                                                                           10 ALGSGVIISKD-GYIVTNNHVIDGADKIKVTIPGSNKEYSATLVGTDSESDLAVIRI-TK 67
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               TOETKRSMRLSDDVQGVLVSQVNENSPAEQAGFRQGNIITKIEEVEVKSVADFNHALEKY
                                                                    25;
      Length 474;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Length 488;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Indels
                                                                Indels
37.3%; Score 722.5; DB 2;
43.5%; Pred. No. 7.3e-37;
ive 74; Mismatches 113;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    37.3%; Score 722.5; DB 2;
40.0%; Pred. No. 7.7e-37;
ive 82; Mismatches 134;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Superfamily: Helicobacter serine proteinase
                                                                Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    -SKPS-VLALNIQRG 465
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    KGKPKRFLVLDLNQG 380
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Best Local Similarity
Matches 158; Conserva
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Status: preliminary
A:Molecule type: DNA
A:Residues: 1-488 <STO>
                                   Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Query Match
      Query Match
                                   Best Loca
Matches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                291
                                                                                                                                                                                                                                                   9
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         188
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         306
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   400
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              453
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       57
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  117
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        282
                                                                                                                                                                                                                                                   ò
                                                                                                                                                                                                                                                                                                             셤
                                                                                                                                                                                                                                                                                                                                                                              ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                셤
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              δ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        g
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ò
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   q
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ò
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               δ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         g
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ð
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           q
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ŏ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Q
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ò
```

7;

Gaps

21;

```
Superfamily: Helicobacter serine proteinase
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               KGKPKRFLVLDLNQG 380
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        -SKPS-VLALNIQRG 466
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      A; Gene: htrA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                246
                                            2
                                                                                                                                                                                                                                                                                                                                                                                                                                              188
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             454
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    99
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  232
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      188
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    292
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      246
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    352
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     306
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                RESULT 14
                                                                                                       g
                                                                                                                                                                                                                                   q
                                                                                                                                                                                                                                                                                                                                                                            g
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ద
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ò
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           g
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ò
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             셤
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             g
                                                                                                                                                                                                                                                                                                              ó
                                                                                                                                                                                                                                                                                                                                                                                                                                                 á
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ò
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   셤
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ò
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               g
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ŏ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  g
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ò
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 d
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ò
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             g
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ò
R; Kalman, S.; Mitchell, W.; Marathe, R.; Lammel, C.; Fan, J.; Olinger, L.; Grimwood, J.; Nature Genet. 21, 385-389, 1999
A; Title: Comparative genomes of Clamydia pneumoniae and C. trachomatis.
A; Reference number: A72000; MUID:99206606; PMID:10192388
A; Accession: G72011
A; Status: preliminary
A; Molecule type: DNA
A; Residues: 1-488 < ARN>
A; Residues: 1-488 < ARN>
A; Residues: 1-488 < ARN>
A; Cross-references: GB-AE001678; GB:AE001363; NID:94377301; PIDN:AAD19116.1; PID:943773C
C; Genetics:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Parkhill, J.; Dougan, G.; James, K.D.; Thomson, N.R.; Pickard, D.; Wain, J.; Churcher, th. T.; Connerton, P.; Cronin, A.; Davis, P.; Davies, R.M.; Dowd, L.; White, N.; Farrar, S.; Moule, S.; O'Gaora, P. Nature 413, 848-852, 2001
A.Authors: Parry, C.; Quail, M.; Rutherford, K.; Simmonds, M.; Skelton, J.; Stevens, K.; A.; Title: Complete genome sequence of a multiple drug resistant Salmonella enterica seroy A. Accession: AC0528
A.Accession: AC0529
A.Accession: AC0528
A.Accession: AC0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           protease Do precursor, heat shock protein HtrA [imported] - Salmonella enterica subsp. C; Species: Salmonella enterica subsp. enterica serovar Typhi A; Note: this species has also been called Salmonella typhi Latte: 09-Nov-2001 #sequence_revision 09-Nov-2001 #text_change 27-Nov-2001 Accession: AC0528
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              7;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     9
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 | |::|::|| || :: :: :|:|| | :| :| :| | 395 -QRVGIRVQNLTPETAKKLGIAPETKGILIISVEPGSVAASSGIAPGQLILAVNRQKVSS 453
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ESDLAVIRITKDNLPTIKFSDSNDISVGDLVFAIGNPFGVGESVTQGIVSALNKSGIGIN 116
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 SYENFIQTDASINPGNSGGALIDSRGGLVGINTAIISKTGGNHGIGFAIPSNMVKDTVTQ 176
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                282 LIRDGQVTRGFLGVTLQPIDAELAACYKLEKVYGALVTDVVKGSPADKAGLKQEDVIIAY 341
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               295 GQLNGLQVEDLTQETKRSMRLSDDVQGVLVSQVNENSPAEQAGFRQGNIITKIEEVEVKS 354
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            2 IPKER-----MERALGSGVIISKDGYIVTNNHVIDGADKIKVTIPGSNKEYSATLVGTDS 56
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      177 LIKTGKIERGYLGVGLQDLSGDLONSY--DNKEGAVVISVEKDSPAKKAGILVWDLITEV
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                235 NGKKVKNTNELRNLIGSMLPNQRVTLKVIRDKKERAFTLTLAERKNPNKKETISAQNGAQ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              21;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     25;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Query Match 37.3%; Score 722.5; DB 2; Length 488; Best Local Similarity 40.0%; Pred. No. 7.7e-37; Matches 158; Conservative 82; Mismatches 134; Indels 21
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Length 475;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Query Match 37.0%; Score 717.5; DB 2; Best Local Similarity 43.2%; Pred. No. 1.5e-36; Matches 162; Conservative 74; Mismatches 114;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        : | | | | : | : | | : | 454 IEDLNRTL---KDSNNENILLMVSQGDVIRFIALK 485
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              355 VADFNHALEKYKGKPKRFLVLDLNQG--YRIILVK 387
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          C;Genetics:
A;Gene: STY0231
C;Superfamily: Helicobacter serine proteinase
                                                                                                                                                                                                                                                                                                                                                                         A;Gene: htrA
C;Superfamily: Helicobacter serine proteinase
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           27
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              117
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   RESULT 13
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      q
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            a
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ద
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          a
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ð
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ద
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              å
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ò
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           õ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ò
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ò
```

heat shock protein htra - Salmonella typhimurium
C; Species: Salmonella typhimurium
C; Species: Salmonella typhimurium
C; Species: Salmonella typhimurium
C; Species: 10-Sep-1999 #text_change 10-Sep-1999
C; Accession: S15377; S21327
R; Johnson, K.; Charles, I.; Dougan, G.; Pickard, D.; O'Gaora, P.; Costa, G.; Ali, T.
Mol. Microbiol. 5, 401-407, 1991
A; Title: The role of a stress-response protein in Salmonella typhimurium virulence. A; Reference number: S15337; MUID:91251770; PMID:1645840
A; Residues: 1-475 CCOS>
A; Residues: 1-475 CCOS>
A; Cross-references: EMBL:X54548; NID:947929; PID:947930
C; Genetics: õ 245 RNLIGSMLPNQRVTLKVIRDKKERAFTLTLAERKNPNKKETISAQNGAQGQLNGLQVEDL 305 245 DNLPTIKFSDSNDISVGDLVFAIGNPFGVGESVTQGIVSALNKSGIGINSYENFIQTDAS 127 128 INPGNSGGALIDSRGGLVGINTAIISKTGGNHGIGFAIPSNMVKDTVTQLIKTGKIERGY 187 RNLIGSMLPNQRVTLKVIRDKKERAFTLTLAERKNPNKKETISAQNGAQGQLNGLQVEDL 305 RAQVGTMPVGSKISLGLLREGK--AITVNL-------ELQQSSQSQVDSSTIFSG 397 TQETKRSMRLSDDVQGVLVSQVNENSPAEQAGFRQGNIITKIEEVEVKSVADFNHALEKY 365 10 ALGSGVII-SKDGYIVTNNHVIDGADKIKVTIPGSNKEYSATLVGTDSESDLAVIRI-TK 67 128 INPGNSGGALIDSRGGLVGINTAIISKTGGNHGIGFAIPSNMVKDTVTQLIKTGKIERGY 292 LGIMGTELSSELAKAMKVDAQRGAFVSQVMPNSSAAKAGIKAGDVITSLNGKPISSFAAL | :|:| ::| ::| ::| ::|: | 352 RAQVGTMPVGSKISLGLLREGK-AITVNL------ELQQSSQSQVDSSTIFSG DNLPTIKFSDSNDISVGDLVFAIGNPFGVGESVTQGIVSALNKSGIGINSYENFIQTDAS LGVGLQDLSGDLQNS--YDNKEGAVVISVEKDSPAKKAGILVWDLITEVNGKKVKNTNEL ALGSGVII-SKDGYIVTNNHVIDGADKIKVTIPGSNKBYSATLVGTDSBSDLAVIRI-TK LGVGLQDLSGDLQNS--YDNKEGAVVISVEKDSPAKKAGILVWDLITEVNGKKVKNTNEL Length 475; Indels Query Match 36.9%; Score 714.5; DB 1; Best Local Similarity 42.9%; Pred. No. 2.3e-36; Matches 161; Conservative 75; Mismatches 114;

```
Nature 392, 353-358, 1998

A; Title: The complete genome of the hyperthermophilic bacterium Aquifex aeolicus.
A; Reference number: A70300; MUID:98196666; PMID:9537320
A; Reference number: A70300; MUID:98196666; PMID:9537320
A; Recission: B70426
A; Status: preliminary; nucleic acid sequence not shown; translation not shown
A; Molecule type: DNA
A; Residues: 1-453 < AGF>
A; Cross-references: GB:AE000741; GB:AE000657; NID:92983841; PIDN:AAC07399.1; PID:9298384
A; Experimental source: strain VF5
C; Genetics:
A;                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                C;Species: Aquifex aeolicus
C,Date: 10-Sep-1999 #sequence_revision 10-Sep-1999 #text_change 21-Jul-2000
C;Accession: B70426
R;Deckert, G.; Warren, P.V.; Gaasterland, T.; Young, W.G.; Lenox, A.L.; Graham, D.E.; Ov
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  6
: : | : | :||:|| | ||| | | ::|::|
398 IEGAEMSNKGQD--KGVVVSSVKANSPAAQIGLKKGDVIIGANQQPVKNIAELRKILD-- 453
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          58 SDLAVIRITKDNLPTI-----KFSDSNDISVGDLVFAIGNPFGVGESVTQGIVSALNKSG 112
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               113 IGINSYENFIQTDASINPGNSGGALIDSRGGLVGINTAIISKTGGNHGIGFAIPSNMVKD 172
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      173 TVTQLIKTGKIERGYLGVGLQDLSGDLQNSYDNKEGAVVISVEKDSPAKKAGILVWDLIT 232
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         EVNGKKVKNTNELRNLIGSMLPNQRVTLKVIRDKKERAFTLTLAERKNPNKKETISAQNG 292
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                293 AQGQLNGLQVEDLTQETKRSMRLSDDVQGVLVSQVNENSPAEQAGFRQGNIITKIEEVEV 352
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              26; Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  3 PKERMERALGSGVIISKDG----YIVTNNHVIDGADKIKVTIPGSNKEYSATLVGTDSE 57
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Query Match 36.6%; Score 710; DB 1; Length 453; Best Local Similarity 41.2%; Pred. No. 4e-36; Matches 163; Conservative 81; Mismatches 126; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                     periplasmic serine proteinase (EC 3.4.21.-) - Aquifex aeolicus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        353 KSVADFNHALEKYK--GKPKRFLVLDLNQGYRIILV 386
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Search completed: November 18, 2002, 11:30:06 Job time: 23 secs
                                                                                                                              366 KGKPKRFLVLDLNQG 380
                                                                                                                                                                                                                        454 -SKPS-VLALNIQRG 466
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        233
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ą
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ŏ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          g
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ŏ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        g
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ò
                                               g
                                                                                                                              δ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      g
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                δ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              음
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ò
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ð
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           à
```

. 7.1 • ,

GenCore version 5.1.3 Copyright (c) 1993 - 2002 Compugen Ltd.

- protein search, using sw model OM protein

November 18, 2002, 11:33:31; Search time 22 Seconds Run on:

(without alignments)
1691.092 Million cell updates/sec

US-09-895-913A-120 Perfect score:

1 MIPKERMERALGSGVIISKD.......KPKRFLVLDLNQGYRIILVK 387 Sequence:

OLIGO Gapop 60.0 , Gapext 60.0 coring table:

283224 seqs, 96134422 residues Searched:

0

Word size :

seq length: 0 seq length: 2000000000 Minimum DB : Maximum DB :

Total number of hits satisfying chosen parameters:

Post-processing: Listing first 45 summaries

Database :

PIR_73:*
1: pir1:*
2: pir2:*
3: pir3:*
4: pir4:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

serine proteinase	serine proteinase	probable/serine pr	proteinase DO VC05	probable serine pr	Degraph protease lik	DO serine proteina	serine proteinase,	do serine proteina	proteinase do (EC	serine proteinase	probable serine pr	probable htrA prot	serine proteinase	serine proteinase	serine proteinase
B70092	F84152	T45448	F82307	C70821	B95338	н86612	G81528	G72011	AG3328	F87590	T45197	B70508	E95261	B98127	A69643
7	~	~	N	7	N	7	7	~	7	~	~	7	7	7	7
400	406	452	456	464	468	488	488	488	524	530	533	549	393	397	449
2.6	5.6	2.6	5.6	5.6	5.6	2.6	5.6	2.6	2.6	5.6	2.6	5.6	2.3	2.3	2.3
10	10	10	10	10	10	10	10	10	10	10	10	10	6	6	6
30	31	32	33	34	35	36	37	38	33	40	41	42	43	44	45

ALIGNMENTS

RESULT 1 C64647

serine proteinase (EC 3.4.21) - Helicobacter pylori (strain 26695)
C;Species: Helicobacter pylori
C;Date: 10-Sep-1999 #sequence_revision 10-Sep-1999 #text_change 09-Jun-2000
C; Accession: C64647
R; Tomb, J.F.; White, O.; Kerlavage, A.R.; Clayton, R.A.; Sutton, G.G.; Fleischmann, R
Peterson, S.; Loftus, B.; Richardson, D.; Dodson, R.; Khalak, H.G.; Glodek, A.; McKer
son, J.D.; Kelley, J.M.; Cotton, M.D.; Weidman, J.M.; Fujii, C.; Bowman, C.; Watthey,
Nature 388, 539-547, 1997
A; Authors: Wallin, E.; Hayes, W.S.; Borodovsky, M.; Karpk, P.D.; Smith, H.O.; Fraser,
A; Title: The complete genome sequence of the gastric pathogen Helicobacter pylori.
A; Reference number: A64520; MUID:97394467; PMID:9252185
A; Accession: C64647
A;Status: preliminary; nucleic acid sequence not shown; translation not shown

A; Molecule type: DNA A; Residues: 1-443 <TON> A; Cross Judices: GB:AE000610; GB:AE000511; NID:92314160; PIDN:AAD08063.1; PID:9231 C; Genetics: GB:AE000610; GB:AE000511; NID:92314160; PIDN:AAD08063.1; PID:9231 C; Superfamily: Holicobacter serine proteinase C; Superfamily: Holicobacter serine proteinase

ö Gaps ö Length 443; Indels ö DB 1; 100.0%; Score 387; Dilarity 100.0%; Pred. No. 0; Conservative 0; Mismatches Similarity Query Match Best Local Simi Matches 387;

1 MIPKERMERALGSGVIISKDGYIVTNNHVIDGADKIKVTIPGSNKEYSATLVGTDSESDL 60 g

AVIRITKDNLPTIKFSDSNDISVGDLVFAIGNPFGVGESVTQGIVSALNKSGIGINSYEN 120 61 ò g

121 FIQTDASINPGNSGGALIDSRGGLVGINTAIISKTGGNHGIGFAIPSNMVKDTVTQLIKT 180 ŏ

셤 g ò

241 NTNELRNLIGSMIPNQRVTLKVIRDKKERAFTLTLAERKNPNKKETISAQNGAQGQLNGL 300 g ŏ

QVEDLTQETKRSMRLSDDVQGVLVSQVNENSPAEQAGFRQGNIITKIEEVEVKSVADFNH 360 301 ŏ g

361 ALEKYKGKPKRFI, VLDLNQGYRIILVK 387 ò

```
C.; Date: 18-Aug-2000 #sequence_revision 20-Aug-2000 #text_change 02-Sep-2000 C; Accession: D82806 Figure 18-Aug-2000 #sequence_revision 20-Aug-2000 #text_change 02-Sep-2000 C; Accession: D82806 Figure 106, 151-157, 2000
A; Title: The genome sequence of the plant pathogen Xylella fastidiosa.
A; Reference number: A82515; MuID:20365717; PMID:10910347
A; Note: for a complete list of authors see reference number A59328 below
A; Accession: D82806
A; Status: preliminary
A; Molecule type: DNA
A; Cross references: Glabourgh B; Arruda, P; Abreu, F.A.; Acencio, M.; Alvarenga, R; Experimental source: strain 9a5c
A; Experimental source: strain 9a5c
B; Simpson, A.J. G; Rednach, F.C.; Arruda, P.; Ferreira, A.J.S.
Submitted to GenBank, June 2000
A; Authors: Ferreira, A.L.B. N. F. Ferreira, J. P.; Franca, S.C.; Franco, M.C.; Fr
J.D.; Junqueira, M.L.; Kemper, E.L.; Kitajima, J.P.; Krieger, J.E.; Kuramae, E.E.; La chado, M.A.; Madella, M. M. S., Matchors: Martins E.M.F.; Matsukuma, A.Y.; Menck, C.F.M.; Miracca, E.C.; Miyaki, C., F.G.; Nunes, L.R.; Oliveira, M.A.; de Oliveira, A.M.B.; Matchors: de Silva, A.C.; Save A; Authors: de Silva, A.C.; Residence number: AS9328
A; Authors: de Silva, A.C.R.; de Silva, A.; Verjovski-Almeida, S.; Vettore, A. C., Concents: Ancolecule A; Accents: Ancolecule A; Accents A; Accent
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Cyncueszoum A. Setubal, J.C.; Kaul, R.; Monks, D.; Chen, L.; Wood, G.E.; Chen, Y.; Woo erage, G.; Gillet, W.; Grant, C.; Guenthner, D.; Kutyavin, T.; Levy, R.; Li, M.; McCl science 294, 2317-2333, 2001
A; Authors: Yoo, H.; Tao, Y.; Biddle, P.; Jung, M.; Krespan, W.; Perry, M.; Gordon-Kam A; Title: The Genome of the Natural Genetic Engineer Agrobacterium tumefaciens C58.
A; Reference number: AB2577; PMID:11743193
A; Accession: ALT3811
A; Status: preliminary
A; Molecule type: DNA
A; Residues: 1 468 < VUR>
A; Residues: 1 468 < VUR>
A; Residues: 1 468 < VUR>
A; Residues: 1 2 468 < VUR>
A; Residues: 1 468 < VURS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Dupont)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       serine proteinase htrA [imported] - Agrobacterium tumefaciens (strain C58, I C;Species: Agrobacterium tumefaciens C;Date: 11-Jan-2002 #sequence_revision 11-Jan-2002 #text_change 17-May-2002 C;Accession: AI2811
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Length 481;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Length 468;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  4.7%; Score 18; DB 2; Le Local Similarity 100.0%; Pred. No. 7.3e-10; les 18; Conservative 0; Mismatches 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              4.4%; Score 17; DB 2; L
100.0%; Pred. No. 7.5e-09;
tive 0; Mismatches 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         A,Gene: XF0285
C,Superfamily: Helicobacter serine proteinase
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     A;Map position: circular chromosome
C;Superfamily: Helicobacter serine proteinase
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          120 NFIQTDASINPGNSGGAL 137
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               222 NFIQTDASINPGNSGGAL 1239
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 203 FIQTDASINPGNSGGAL, 219
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            121 FIQTDASINPGNSGGAL 137
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Best Local Similarity 100.
Matches 17; Conservative
          C; Species: Xylella fastidiosa
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 C;Genetics:
A;Gene: htrA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Best Loca
Matches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             RESULT 5
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                δ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ò
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           g
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Serine proteinase (proteinase DO) (EC 3.4.21.-) Cj1228c [imported] - Campylobacter jejun C;Species: Campylobacter jejuni C;Species: Campylobacter jejuni C;Date: 31-Mar-2000 #sequence_revision 31-Mar-2000 #text_change 03-Jun-2002 C;Accession: F81329 R;Parkhill, J.; Wren, B.W.; Mungall, K.; Ketley, J.M.; Churcher, C.; Basham, D.; Chillin R; Parkhill, J.; Wrea B.W.; Mungall, K.; Ketley, J.M.; VanVliet, A.; Whitehead, S.; Barrel Nature 403, 665-668, 2000 A;Title: The genome sequence of the food-borne pathogen Campylobacter jejuni reveals hyp A;Reference number: A81250; MUID:20150912; PMID:10688204
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  A Status: preliminary
Molecule type: DNA
Molecule type: LNA
Status: 1-472 cPAR>
A. Cross-references: GB:AL139077; GB:AL111168; NID:g6968444; PIDN:CAB73482.1; PID:g696866
A. Experimental source: serotype O2, strain NCTC 11168
                                                                                                                                                                                                                                                                                                 proteinase DO - Helicobacter pylori (strain J99)
(Species: Helicobacter pylori
A; Vatriety: Strain J99
C; Date: 12-Feb-1999 #sequence_revision 12-Feb-1999 #text_change 20-Sep-1999
C; Date: 12-Feb-1999 #sequence_revision 12-Feb-1999 #text_change 20-Sep-1999
C; Date: 12-Feb-1999 #sequence_revision 12-Feb-1999 #text_change 20-Sep-1999
C; Date: 17-Feb-1999 #sequence_revision 12-Feb-1999 #text_change 20-Sep-1999
C; Date: 17-Feb-1999 #text_change 20-Sep-1999
Associated Provision 12-Feb-1999
Assoc
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Aritle: Genomic sequence comparison of two unrelated isolates of the human gastric path A; Reference number: A71800; MUID:99120557; PMID:9923682
A; Accession: H7136
A; Status: preliminary
A; Molecule type: DNA
A; Residues: 1-476 <ARN>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               A;Cross-references: GB:AE001474; GB:AE001439; NID:g4154929; PIDN:AAD05980.1; PID:g415493
A;Experimental source: strain J99
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   174 VTQLIKTGKIERGYLGVGLQDLSGDLQNSYDNKEGAVVISVEKDSPAKKAGILVWDLITE 233
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       RESULT 4
D82826
heat shock protein XF0285 [imported] - Xylella fastidiosa (strain 9a5c)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Query Match 24.8%; Score 96; DB 2; Length 476; Best Local Similarity 100.0%; Pred. No. 8.8e-90; Matches 96; Conservative 0; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       5.2%; Score 20; DB 2; Length 472;
100.0%; Pred. No. 6.4e-12;
.lve 0; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            234 VNGKKVKNTNELRNLIGSMLPNQRVTLKVIRDKKER 269
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      323 VNGKKVKNTNELRNLIGSMLPNQRVTLKVIRDKKER 358
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Superfamily: Helicobacter serine proteinase
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              A)Gene: htrA, Cj1228c
C;Superfamily: Helicobacter serine proteinase
C;Keywords: hydrolase; serine proteinase
118 YENFIQTDASINPGNSGGAL 137
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    210 YENFIQTDASINPGNSGGAL 229
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                20; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  A; Accession: F81329
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Gene: htrA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    C; Genetics:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Matches
                                               g
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             셤
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ò
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     d
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              g
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         à
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ð
```

ന

ö

Gaps

ó;

Length 424;

```
A) Status: preliminary
A) Molecule type: DNA
By Molecule type: By Molecule type: DNA
By Molecule type: By Molecule type: DNA
By Molecule type: By Molecule type: DNA
By Molecule type: Molecule type: DNA
By Molecule type: Molecule type: DNA
By Molecule type: Molecule type: Molecule type: DNA
By Molecule type: Mo
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         heat shock protein htrA - Haemophilus influenzae (strain Rd KW20)
N;Alternate names: periplasmic serine proteinase Do homolog
C;Species: Haemophilus influenzae
C;Date: 10-Sep-1999 #sequence_revision 10-Sep-1999 #text_change 28-Jul-2000
A;Reference number: A89758; MUID:21311952; PMID:11418146
A;Accession: D89957
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Query Match 3.1%; Score 12; DB 2; L. Best Local Similarity 100.0%; Pred. No. 0.00091; Matches 12; Conservative 0; Mismatches 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    117 TNNHVIDGADKI 128
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   25 TNNHVIDGADKI 36
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            22 YIVTNNHVIDGA 33
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 RESULT 10
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ò
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                g
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   οy
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 q
                                                                                                                                                                                                                       htra protein homolog [imported] - Agrobacterium tumefaciens (strain C58, Cereon)

S.Species: Agrobacterium tumefaciens
C;Date: 30-Sep-2001 #sequence_revision 30-Sep-2001 #text_change 17-May-2002
C;Accession: B97590
R;Goodner, B.; Hinlale, G.; Gattung, S.; Miller, N.; Blanchard, M.; Qurollo, B.; Goldman, A.; Liu, F.; Wollam, C.; Allinger, M.; Doughty, D.; Scott, C.; Lappas, C.; Markelz, B.; Science 294, 2323-2328, 2001
A;Title: Genome Sequence of the Plant Pathogen and Biotechnology Agent Agrobacterium tum A;Reference number: A97359; PMID:11743194
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Serine protease Do (heat-shock protein) [imported] - Clostridium acetobutylicum C; Species: Clostridium acetobutylicum C; Spacession: H96556 R; Spacession: H96556 R; Smelling, J.; Breton, G.; Omelchenko, M.V.; Markarova, K.S.; Zeng, Q.; Gibson, R.; Lee, J.; Daly, M.J.; Bennett, G.N.; Koonin, B.V.; Smith, D.R. A; Fille: Genome Sequence and Comparative Analysis of the Solvent-Producing Bacterium Clc A; Fille: Genome Sequence and Comparative Analysis of the Solvent-Producing Bacterium Clc A; Reference number: A96900; MUID:21359325; PMID:21359325 Status: preliminary A; Molecule type: DNA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  hypothetical protein SA1549 [imported] - Staphylococcus aureus (strain N315)
C;Species: Staphylococcus aureus
C;Date: 10-May-2001 #sequence_revision 10-May-2001 #text_change 16-Aug-2002
C;Accession: D89957
R;Kuroda, M.; Ohta, T.; Uchiyama, I.; Baba, T.; Yuzawa, H.; Kobayashi, I.; Cui, L.; Oguc
R;Kuroda, M.; Ohta, T.; Kobayashi, N.; Sawano, T.; Inoue, R.; Kaito, C.; Sekimizu, K.;
C.; Shiba, T.; Hattori, M.; Ogasawara, N.; Hayashi, H.; Hiramatsu, K.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          C; Superfamily: Escherichia coli trypsin-like proteinase; GLGF domain homology; trypsin
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           A; Residues: 1-348 -KUR>
A; Cross-references: GB:AE001437; PIDN:AAK78443.1; PID:g15023321; GSPDB:GN00168
A; Experimental source: Clostridium acetobutylicum A; CC824
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                A; Cross-references: GB: AE007869; PIDN: AAK87675.1; PID: 915157032; GSPDB: GN00169
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       A; Title: Whole genome sequencing of meticillin-resistant Stapylococcus aureus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Query Match 3.6%; Score 14; DB 2; Length 348; Best Local Similarity 100.0%; Pred. No. 6.8e-06; Matches 14; Conservative 0; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Query Match 4.4%; Score 17; DB 2; Length 495; Best Local Similarity 100.0%; Pred. No. 7.9e-09; Matches 17; Conservative 0; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                A;Map position: circular chromosome
C;Superfamily: Helicobacter serine proteinase
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          230 FIQTDASINPGNSGGAL 246
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             121 FIQTDASINPGNSGGAL 137
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                122 IQTDASINPGNSGG 135
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       194 IQTDASINPGNSGG, 207
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               A;Status: preliminary;
Molecule type: DNA
;Residues: 1-495 <KUR>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  C;Genetics:
A;Gene: AGR_C_3507
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        CAC0463
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      C; Genetics:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    RESULT 8
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   δ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      셤
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ò
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         g
```

```
Cydrocession: A64113
R;Fleischmann, R.D.; Adams, M.D.; White, O.; Clayton, R.A.; Kirkness, E.F.; Kerlavage ; Gozaye, J.D.; Scott, J.; Shirley, R.; Liu, L.I.; Glodek, A.; Kelley, J.M.; Weidman ; Gozaye, J.D.; Scott, J.; Shirley, R.; Liu, L.I.; Glodek, A.; Kelley, J.M.; Weidman ; C.D.M.; Brandon, R.C.; Fittchman, J.L.; Fuhrmann, J.L.; Geoghagen, N.S.M.; Arathers: Gnehm, C.L.; MeDonald, L.A.; Small, K.V.; Fraser, C.M.; Smith, H.O.; Vente A; Title: Whole-genome random sequencing and assembly of Haemophilus influenzae Rd. A; Reference number: A64000; MUID:95350630; PMID:7542800
A; Reference number: A64000; MUID:95350630; PMID:7542800
A; Residues: 1-466 < TIGK>
A; Residues: 1-466 < TIGK>
A; Residues: 1-466 < TIGK>
A; Construction of the control of the 
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             htra-like protein - Brucella abortus
C;Species: Brucella abortus
C;Species: Brucella abortus
C;Date: 10.Sep-1999 #sequence_revision 10-Sep-1999 #text_change 21-Jul-2000
C;Accession: I40059
R;Tatum, F.M.; Cheville, N.F.; Morfitt, D.
Microb. Pathog. 17, 23-36, 1994
A;Title: Cloning, characterization and construction of htrA and htrA-like mutants of
A;Reference number: I40059; MUID: 95165990; PMID: 7861951
A;Accession: I40059
A;Status: preliminary; translated from GB/EMBL/DDBJ
A;Molecule type: DNA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            A; Residues: 1474 ARSS-
A; Cross-references: EMEL-U07351 NID:9497154; PIDN:AAA70163.1; PID:9497155
C; Superfamily: Helicobacter serine proteinase
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Query Match 3.1%; Score 12; DB 1; Length 474; Best Local Similarity 100.0%; Pred. No. 0.001; Matches 12; Conservative 0; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Length 466;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Query Match
3.1%; Score 12; DB 1; Lk
Best Local Similarity 100.0%; Pred. No. 0.00099;
Matches 12; Conservative 0; Mismatches 0;
```

```
proteinase DO (EC 3.4.21.-) precursor / heat shock protein htrA - Escherichia coli (s C:Species: Escherichia coli (c:Species: Escherichia coli (c:Species: Escherichia coli (c:Species: Escherichia coli (s C:Species: Escherichia coli seguence_revision 16-Feb-2001 #text_change 17-May-2002 C:Accession: EB5500 R;Perna, N.T.: Plunkett III, G.; Burland, V.; Mau, B.; Glasner, J.D.; Rose, D.J.; May liler, L.; Grotbeck, E.J.; Davis, N.W.; Lim, A.; Dimalanta, E.; Potamousis, K.; Apoda Nature 409, 529-533, 2001 A;Title: Genome sequence of enterohemorrhagic Escherichia coli O157:H7. A;Reference number: A85480; MUID:21074935; PMID:11206551
Proc. Natl. Acad. Sci. U.S.A. 99, 443-448, 2002
A;Title: The genome sequence of the facultative intracellular pathogen Brucella melit
A;Reference number: AD3252; PMID:11756688
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Esche
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           A;Status: preliminary
A;Molecule type: DNA
A;Residues: 1-474 <STO>
A;Cross-references: GB:AE005174; NID:g12512885; PIDN:AAG54465.1; GSPDB:GN00145; UWGP:
A;Experimental source: strain 0157:H7, substrain EDL933
C;Genetics:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    proteinase DO (EC 3.4.21.-) precursor / heat shock protein ECs0165 [imported] - Esch C; Species: Escherichia coli
C; Species: Escherichia coli
C; Date: 18-Jul-2001 #sequence_revision 18-Jul-2001 #text_change 17-May-2002
C; Accession: B90649
R; Hayashi, T; Makino, K; Ohnishi, M.; Kurokawa, K.; Ishil, K.; Yokoyama, K.; Han, gasawara, N.; Yasunaga, T.; Ruhara, S.; Shiba, T.; Hattori, M.; Shinagawa, H. DNA Res. 8, 11-22, 2001
A; Title: Complete genome sequence of enterohemorrhagic Escherichia coli O157:H7 and A; Accession: B90649
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ö
                                                                                                                                                                                                                   A; Molecule type: DNA
A; Residues: 1-474 < KUR>
A; Residues: 1-474 < KUR>
A; Cross-references: GB:AE008917; PIDN:AAL51964.1; PID:g17982723; GSPDB:GN00190
A; Experimental source: strain 16M
C; Genetics:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   A;Status: preliminary
A;Molecule type: DNA
A;Residues: 1-474 <HAY>
A;Cross-references: GB:BA000007; PIDN:BAB33588.1; PID:gl3359621; GSPDB:GN00154
A;Experimental source: strain 0157:87, substrain RIMD 0509952
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ;
0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            DB 2; Lens.
3. 0.001;
0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Length 474;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Length 474;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            DB 2;
0.001;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Query Match 3.1%; Score 12; DB Best Local Similarity 100.0%; Pred. No. 0.0 Matches 12; Conservative 0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Query Match 3.1%; Score 12; DB Best Local Similarity 100.0%; Pred. No. 0.0 Matches 12; Conservative 0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                             A;Map position: I
C;Superfamily: Helicobacter serine proteinase
C;Keywords: hydrolase; serine proteinase
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Superfamily: Helicobacter serine proteinase
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       A,Gene: htrA
C,Superfamily: Helicobacter serine protei
C,Keywords: hydrolase; serine proteinase
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              215 INPGNSGGALID 226
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                128 INPGNSGGALID 139
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          160 GIGFAIPSNMVK 171
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        263 GIGFAIPSNMVK 274
                                                                                                                                                                                         A;Status: preliminary
                                                                                                                                         A; Accession: AI3349
                                                                                                                                                                                                                                                                                                                                                                                                                                  A; Gene: BMEI0783
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           RESULT 13
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     RESULT 14
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          g
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ò
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ò
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        q
                                                                                                                                                                                                                                                                                            proteinase DO (EC 3.4.21.-) precursor / heat shock protein htrA - Escherichia coli (Stra C) bate: 13.4an-1995 #sequence_revision 13.4an-1995 #text_change 01-mar-2002 (S. Accession: S45229; A64740; S01899; B35993 (S. Fujita, N. Submitted to the EMBL Data Library, January 1994 (S. Fujita, N. S. Escherichia Library, January 1994 (S. Fujita, N. S. Escherichia Library, January 1994 (S. Fujita, N. S. Escherichia Coli R. Fujita, N. Statichia Coli R. Fujita, N. Statichia Coli R. S. Fujita, N. Statichia Coli R. S. Fujita, S. Scherichia Coli R. S. Scherichia Coli R. S. Statichia Coli R. Statichia Col
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      A; Molecule type: DNA
A; Residues: 1-9, 'R',11-191, 'G',193-466, 'RHLPVNAVISLNPFLKTGRGSPYNL' <LIP>
A; Residues: 1-9, 'R',11-191, 'G',193-466, 'RHLPVNAVISLNPFLKTGRGSPYNL' <LIP>
A; Cross-references: EMBL: X1245; NID:941760; PIDN:CA30997.1; PID:941761
A; Experimental source: strain K-12
B; Wurgler, S.M.; Richardson, C.C.
B; Wurgler, S.M.; Richardson, C.C.
A; Tutle: Structure and regulation of the gene-for dGTP triphosphohydrolase from Escheric A; Reference number: A35993; MUID:90207273; PMID:2157212
A; Accession: B35993
A; Status: preliminary
A; Molecule type: DNA
A; Residues: 1-9, 'R', 11-16 <WUR>
A; Residues: 1-9, 'R', 11-16 <WUR>
A; Cross-references: GB:M31772; NID:9145733; PIDN:AAA23680.1; PID:9145736
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               proteinase DO (EC 3.4.21.-) [imported] - Brucella melitensis (strain 16M)
C;Species: Brucella melitensis
C;Species: Ol'Feb-2002 #sequence_revision 01-Feb-2002 #text_change 15-Feb-2002
C;Accession: A13349
R;DelVecchio, V.G.; Kapatral, V.; Redkar, R.J.; Patra, G.; Mujer, C.; Los, T.; Ivanova, Mazur, M.; Goltsman, E.; Selkov, E.; Elzer, P.H.; Hagius, S.; O'Callaghan, D.; Letess
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            A; Molecule type: DNA
A; Residues: 1-474 <BLAT>
A; Residues: 1-474 <BLAT>
A; Residues: 1-474 <BLAT>
A; Cross-references: GB + AE000125; GB: U00096; NID: 91786348; PIDN: AAC73272.1; PID: 91786356; A; Lipinska, B.; Sharma, S.; Georgopoulos, C.
Nucleic Acids Res. 16, 10053-10067
A; Title: Sequence analysis and regularized of the hira gene of Escherichia coli: a sigma(A; Reference number: S01899; MUID: 89057448; PMID: 3057437
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ;
0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          11-26/Domain: signal sequence #status predicted <SIG>
27-474/Product: heat shock protein htrA #status predicted <MAT>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Title: The complete genome sequence of Escherichia coli K-12. Reference number: A64720; MUID:97426617; PMID:9278503 Accession: A64740 Status: nucleic acid sequence not shown; translation not shown
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       3.1%; Score 12; DB 2; Length 474; ilarity 100.0%; Pred. No. 0.001; Conservative 0; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           A)Gene: htrA
A,Map position: 4 min
C,Superfamily: Helicobacter serine proteinase
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Keywords: hydrolase; serine proteinase
            128 INPGNSGGALID 139
                                                        215 INPGNSGGALID 226
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           160 GIGFAIPSNMVK 171
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      263 GIGFAIPSNMVK 274
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Query Match
Best Local Similarity
Matches 12; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        C;Genetics
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      RESULT 12
                                                                                                                                                                                                                           RESULT 11
                                                                                              셤
            õ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ŏ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Q
```

```
heat shock protein htra - Salmonella typhimurium
C; Species: Sissis Sesquence_revision 10-Sep-1999 #text_change 10-Sep-1999
C; Accession: Sissis Session: Sissis Session: Sissis Session: Sissis Session: Sissis Session: Sissis Mulb:91251770; PMID:1645840
A; Reference number: Sissis Mulb:91251770; PMID:1645840
A; Residues: 1-475 <COS>
A; Residues: 1-475 <COS>
A; Cross-references: EMBL:X54548; NID:947929; PID:947930
                                                                                                                                                                    ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ö
                                                                                                                                                                       Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 0; Gaps
                                                                                                                                                                  ;
                                                                                                      Query Match
3.1%; Score 12; DB 2; Length 474;
Best Local Similarity 100.0%; Pred. No. 0.001;
Matches 12; Conservative 0; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Query Match 3.1%; Score 12; DB 1; Length 475; Best Local Similarity 100.0%; Pred. No. 0.001; Matches 12; Conservative 0; Mismatches 0; Indels
A;Gene: ECs0165
C;Superfamily: Helicobacter serine proteinase
C;Keywords: hydrolase; serine proteinase
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  C; Superfamily: Helicobacter serine proteinase
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Search completed: November 18, 2002, 11:35:56 Job time: 23 secs
                                                                                                                                                                                                                        160 GIGFAIPSNMVK 171
                                                                                                                                                                                                                                                    1111111111
263 GIGFAIPSNMVK 274
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 160 GIGFAIPSNMVK 171
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    11111111111
264 GIGFAIPSNMVK 275
                                                                                                                                                                                                                                                                                                                                                          RESULT 15
S15337
                                                                                                                                                                                                                                                                     q
                                                                                                                                                                                                                        ò
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       õ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     q
```

*• · · ·

```
November 18, 2002, 11:30:11; Search time 40 Seconds (without alignments)
1289.200 Million cell updates/sec
                                                                                                                                                                                             US-09-895-913A-120
387
1 MIPKERMERALGSGVIISKD......RPKRFLVLDLNQGYRIILVK 387
                                                                                                                                                                                                                                                                                                                                                                                                                      908470
GenCore version 5.1.3 Copyright (c) 1993 - 2002 Compugen Ltd.
                                                                                                                                                                                                                                                                                                                                                                                                                    Total number of hits satisfying chosen parameters:
                                                                                                                                                                                                                                                                                                                                        908470 seqs, 133250620 residues
                                                                              OM protein - protein search, using sw model
                                                                                                                                                                                                                                                                              OLIGO
Gapop 60.0 , Gapext 60.0
                                                                                                                                                                                                                                                                                                                                                                                                                                                       Minimum DB seq length: 0
Maximum DB seq length: 200000000
                                                                                                                                                                                                                                                                                                                                                                             0
                                                                                                                                                                                               Title:
Perfect score:
Sequence:
                                                                                                                                                                                                                                                                              Scoring table:
                                                                                                                                                                                                                                                                                                                                                                               Word size :
                                                                                                                                                                                                                                                                                                                                        Searched:
                                                                                                                   Run on:
```

Post-processing: Listing first 45 summaries

Database

 A_Ge	A_Geneseq_101002:*
1: /	/SIDS2/gcgdata/geneseg/genesegp-embl/AA1980.DAT:*
5:	/SIDS2/gcgdata/geneseg/genesegp-embl/AA1981.DAT:*
3:	/SIDS2/gcgdata/geneseq/geneseqp-embl/AA1982.DAT:*
4:	<pre>'SIDS2/gcgdata/geneseq/geneseqp-emb1/AA1983.DAT:*</pre>
2:	'SIDS2/gcgdata/geneseg/genesegp-embl/AA1984.DAT:*
9:	'SIDS2/gcgdata/geneseq/genesegp-emb1/AA1985.DAT:*
7: /	/SIDS2/gcgdata/geneseg/genesegp-emb1/AA1986.DAT:*
8:	/SIDS2/gcgdata/geneseg/genesegp-embl/AA1987.DAT:*
6	/SIDS2/gcgdata/geneseg/genesegp-embl/AA1988.DAT:*
10:	/SIDS2/gcgdata/geneseg/genesegp-embl/AA1989.DAT:*
11:	/SIDS2/gcgdata/geneseg/genesegp-embl/AA1990.DAT:*
12:	/SIDS2/gcgdata/geneseg/genesegp-embl/AA1991.DAT:*
13:	/SIDS2/gcgdata/geneseq/geneseqp-embl/AA1992.DAT:*
14:	/SIDS2/gcgdata/geneseg/genesegp-embl/AA1993.DAT:*
15:	/SIDS2/gcgdata/geneseg/genesegp-embl/AA1994.DAT:*
16:	/SIDS2/gcgdata/geneseq/genesegp-embl/AA1995.DAT:*
17:	/SIDS2/gcgdata/geneseg/genesegp-embl/AA1996.DAT:*
18:	/SIDS2/qcqdata/qeneseq/qeneseqp-embl/AA1997.DAT:*
19:	/SIDS2/gcgdata/geneseq/geneseqp-embl/AA1998.DAT:*
50:	/SIDS2/gcgdata/geneseg/genesegp-embl/AA1999.DAT:*
21:	/SIDS2/gcgdata/geneseg/genesegp-embl/AA2000.DAT:*
22:	/SIDS2/gcgdata/geneseg/genesegp-embl/AA2001.DAT:*
23:	/SIDS2/gcgdata/geneseg/genesegp-emb1/AA2002.DAT:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Description		H. pylori GHPO 536	Antigen 1 from clu	Expressed antigen	Protein encoded by	Protein encoded by	Lawsonia intracell	S. typhimurium Htr	Escherichia coli s	Novel human diagno	Streptococcus poly
GI.		Q,	AAW89850	AAW89984	AAW89977	AAW89817	AAG78605	AAR14625	AAW56771	ABG25263	ABP27963
80	:	19	20	20	20	20	22	12	19	22	23
% Query e Match Length DB I		387	443	288	451	187	474	475	491	168	380
% Query Match		100.0	79.3	74.4	42.6	27.1	3.4	3.1	3.1	2.8	2.8
Score		387	307	288	165	105	13	12	12	11	11
Result No.		1	7	æ	4	ഗ	9	7	80	6	10

The HtrA surface p Lactococcus lactis Group B Streptococcus poly Streptococcus poly Streptococcus poly Streptococcus poly E. coli growth and Listeria monocytog Heat shock protein Novel human diagno Novel human diagno Novel human procease. It Chlamydia pneumoni S. epidermidis ope Propionipacterium Streptococcus poly Staphylococcus epi BASB011 protein se Mycobacterium tube Mycobacterium tube Mycobacterium tube My tuberculosis in My tuberculosis ne	cubacterium sp sobacterium sp JP protease. reptococcus pn JP protease ca
21 AAY93768 23 ABB55490 23 AAB55490 23 AAB79845 23 AAB79845 22 AAG89846 22 AAG77434 22 AAG77434 22 AAG79110 22 AAG79110 22 AAG79110 22 AAG79113 22 AAG81365 21 AAY59354 21 AAY59354 22 AAG81139 22 AAG81139 23 AAG8139 24 AAY9955 26 AAY99564 27 AAY99664 28 AAY99664 29 AAY39968 20 AAY39968 20 AAY39968 20 AAY39968 20 AAY39968 20 AAY39968	
	00668
11121111111111111111111111111111111111	7 4 4 4 4 7 4 6 4 6 9 4 6 4 6

ALIGNMENTS

```
GHPO protein; Helicobacter infection; gastroduodenal disease; gastritis; peptic ulcer disease.
RESULT 1
AAW98445
ID AAW98445 standard; Protein; 387 AA.
                                                                                                                                                                                H. pylori GHPO 536 protein.
                                                                                                                                       31-MAR-1999 (first entry)
                                                                                          AAW98445;
```

97ttS-0902615. 97ttS-0833457. 97ttS-0881227. 98WO-US06371. Helicobacter pyloxi. 29-JUL-1997; 01-APR-1997; 24-JUN-1997; 01-APR-1998; WO9843478-A1 08-OCT-1998.

(HUMA-) HUMAN GENOME SCI INC. (INMR) MERIEUX ORAVAX PASTEUR MERIEUX SERUMS.

Tomb J; Oomen RP, Al-Garawi A, Kleanthous H, Miller C, WPI; 1998-542293/46. N-PSDB; AAX14164.

```
ò
                                                                                                                                                                                                                                                                                                    a
                                                                                                                                                                                                                                                                                                                                       g
                                                                                                                                                                                                                                                                                                                                                                            셤
                                                                                                                                                                                                                                                                                                                                                                                                                g
                                                                                                                                                                                                                                                                                                                                                                                                                                                     g
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        à
                                                                                                                                                                                                                                                                                                                                                          ò
                                                                                                                                                                                                                                                                                                                                                                                               ö
                                                                                                                                                                                                                                                                                                                                                                                                                                    à
                                                                                                                                                                                                                                                                                                                                                                                                                                                                        à
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         d
                                                                                                                                                                       ö
                                                                                              þe
                                                      This sequence represents a Helicobacter pylori GHPO protein of the invention. The polypeptides can be used for preventing or treating Helicobacter infections, and gastroduodenal diseases associated with these infections, including acute, chronic, and atrophic gastritis, and peptic ulcer diseases, e.g. gastric and duodenal ulcers. They can also be used for the production of antibodies. The products can also be used for
                                                                                                                                                                                                                                                                                                                                     AVIRITKDNLPTIKFSDSNDISVGDLVFAIGNPFGVGESVTQGIVSALNKSGIGINSYEN 120
                                                                                                                                                                                                                                    121 FIQTDASINPGNSGGALIDSRGGLVGINTAIISKTGGNHGIGFAIPSNMVKDTVTQLIKT 180
                                                                                                                                                                                                                                                                                  180
                                                                                                                                                                                                                                                                                                  GKIERGYLGVGLQDLSGDLQNSYDNKEGAVVISVEKDSPAKKAGILVWDLITEVNGKKVK 240
                                                                                                                                                                                                                                                                                                                      240
                                                                                                                                                                                                                                                                                                                                                                           QVEDLIQETKRSMRLSDDVQGVLVSQVNENSPAEQAGFRQGNIITKIEEVEVKSVADFNH 360
                                                                                                                                                                                                                                                                                                                                                                                     Gaps
                                                                                                                                                                                                         9
New isolated Helicobacter polynucleotides - used to develop products for the diagnosis, prevention and treatment of Helicobacter
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        diagnosis;
                                                                                                                                                                                                 1 MIPKERMERALGSGVIISKDGYIVTNNHVIDGADKIKVTIPGSNKEYSATLVGTDSESDL
                                                                                                                                                                                      MIPKERMERALGSGVIISKDGYIVTNNHVIDGADKIKVTIPGSNKEYSATLVGTDSESDL
                                                                                                                                                                                                                                                                         ö
                                                                                                                                                   Length 387;
                                                                                                                                                                      Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Antigen; immunogenic cluster family; vaccine; gastritis; peptic ulcer; gastric adenocarcinoma; gastric lymphoma.
                                                                                                                                                   DB 19;
                                                                                                                                                                    ö
                                                                                                                                                 100.0%; Score 387; 1
100.0%; Pred. No. 0;
                                                                                                                                                                    0; Mismatches
                infections and gastrointestinal diseases
                                   8; Page 769-771; 2054pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                               361 ALEKYKGKPKRFLVLDLNQGYRIILVK 387
                                                                                                                                                                                                                                                                                                                                                                                                                         Ä.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                               AAW89850 standard; Protein; 443
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           97US-0061958
97US-0045107
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          98WO-US08487
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Antigen 1 from cluster 04a.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    (first entry)
                                                                                                                                                                     Conservative
                                                                                                              detection and diagnosis
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Antigen; immunogenic
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Helicobacter pylori
                                                                                                                                                           al Similarity
387; Conserv
                                                                                                                                 387 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    WO9849314-A2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    18-FEB-1999
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         27-APR-1998;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            14-OCT-1997;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    25-APR-1997;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       05-NOV-1998
                                                                                                                                 Seguence
                                                                                                                                                 Query Match
Best Local S
Matches 387
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 AAW89850;
                                    Claim
                                                                                                                                                                                                                                                                                                                                                        241
                                                                                                                                                                                                                          61
                                                                                                                                                                                                                                            61
                                                                                                                                                                                                                                                                                                                                       241
                                                                                                                                                                                                                                                                                                                                                                          301
                                                                                                                                                                                                                                                                                                                                                                                                                                 361
                                                                                                                                                                                                                                                                                                  181
                                                                                                                                                                                                                                                                                                                                                                                                                                                             RESULT 2
AAW89850
ID AAW8
g
                                                                                                                                                                                       õ
                                                                                                                                                                                                       a
                                                                                                                                                                                                                          à
                                                                                                                                                                                                                                                                              QQ
                                                                                                                                                                                                                                                                                                                 8
                                                                                                                                                                                                                                                                                                                                                                                           8
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        g
                                                                                                                                                                                                                                                             ò
                                                                                                                                                                                                                                                                                                  à
                                                                                                                                                                                                                                                                                                                                     δ
                                                                                                                                                                                                                                                                                                                                                       g
                                                                                                                                                                                                                                                                                                                                                                          ò
```

```
ö
                                                                                                                                                                                                                                                                                                                        The present sequence represents a Helicobacter pylori antigenic protein that is characterised by immunoreactivity with H. pylori-positive antisera. The proteins are highly immunogenic and induce a long-lasting immune response that persists even after antimicriobial treatment. In antibody-detection assays, on sera, plasma, urine, saliva etc., they are highly sensitive and specific. The specification also describes 69 previously unrecognised immunogenic cluster families. H. pylori antigens are used to detect H. pylori-specific antibodies, for diagnosing infection or to confirm eradication of infection, and in vaccines to protect against H. pylori infection and related diseases (gastritis, peptic ulcer, gastric adenocarcinoma/lymphoma).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          GKIERGYLGVGLQDLSGDLQNSYDNKEGAVVISVEKDSPAKKAGILVWDLITEVNGKKVK 240
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             AVIRITKDNLPTIKFSDSNDISVGDLVFAIGNPFGVGESVTQGIVSALNKSGIGINSYEN 120
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               241 NTNELRNLIGSMLPNQRVTLKVIRDKKERAFTLTLAERKNPNKKETISAQNGAQGQLNGL 300
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Gaps
                                                                                                                                                                New Helicobacter pylori antigens and related nucleic acid sequences - useful in serological diagnosis and protective vaccines, providing
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Antigen; immunogenic cluster family; vaccine; gastritis; diagnosis; peptic ulcer; gastric adenocarcinoma; gastric lymphoma.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        121 FIQTDASINPGNSGGALIDSRGGLVGINTAIISKTGGNHGIGFAIPSNMVKDTVTQLIKT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Length 443;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   79.3%; Score 307; DB 20;
100.0%; Pred. No. 2.5e-307;
ive 0; Mismatches 0;
                                                                                                                                                                                                                                                                             English.
                                                      McAtee CP;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       AAW89984 standard; Protein; 288 AA
(GENE-) GENELABS TECHNOLOGIES INC.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Expressed antigen for clone Y261A.
                                                                                                                                                                                                                                                                          Claim 1; Page 211-212; 402pp;

    useful in serological diagr
    long-lasting immune response

                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Query Match 79.3°
Best Local Similarity 100.
Matches 307; Conservative
                                                         E I
                                                                                                       WPI; 1999-009433/01
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Helicobacter pylori.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     443 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            |||||||||||
QVEDLTQ 363
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         301 QVEDLTQ 307
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     WO9849314-A2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 18-FEB-1999
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        05-NOV-1998
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             61
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     181
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                357
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   RESULT 3
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             AAW89984
```

```
Chow TP,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        AAW89817;
                                                                                                                                                                                                                                                                                                                                                                             Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     121
                                                                                                                                                                                                                                                                                                                                                                                                                                                                   65
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        61
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          185
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             RESULT 5
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      AAW89817
 g
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        õ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              g
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     à
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        qq
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ð
                                                                                                                                                                                                                                                                                                                                                                                      ó
                                                                                                                                                                                                The present sequence represents a Helicobacter pylori antigenic protein that is characterised by immunoreactivity with H. pylori-positive antisera. The proteins are highly immunogentc and induce a long-lasting immuno response that persists even after antimicriobial treatment. In antibody-detection assays, on sera, plasma, urine, saliva etc., they are highly sensitive and specific. The specification also describes 69 previously unrecognised immunogenic cluster families. H. pylori antigens are used to detect H. pylori-specific antibodies, for diagnosing infection or to confirm eradication of infection, and in vaccines to protect against H. pylori infection and related diseases (gastritis, peptic ulcer, gastric adenocarcinoma/lymphoma).
                                                                                                                                                                                                                                                                                                                                                                                                          100 VTQGIVSALNKSGIGINSYENFIQTDASINPGNSGGALIDSRGGLVGINTAIISKTGGNH 159
                                                                                                                                                                                                                                                                                                                                                                                                                                                                   121 AKKAGILVWDLITEVNGKKVKNTNELRNLIGSMLPNORVTLKVIRDKKERAFTLTLAERK 180
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            GIGFAIPSNMVKDTVTQLIKTGKIERGYLGVGLQDLSGDLQNSYDNKEGAVVISVEKDSP 219
                                                                                                                                                                                                                                                                                                                                                                                      Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                 9
                                                                                                                                   New Helicobacter pylori antigens and related nucleic acid sequences useful in serological diagnosis and protective vaccines, providing
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Antigen; immunogenic cluster family; vaccine; gastritis; diagnosis; peptic ulcer; gastric adenocarcinoma; gastric lymphoma.
                                                                                                                                                                                                                                                                                                                                                                                                                       1 VTQGIVSALNKSGIGINSYENFIQTDASINPGNSGGALIDSRGGLVGINTAIISKTGGNH
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    AKKAGILVWDLITEVNGKKVKNTNELRNLIGSMLPNQRVTLKVIRDKKERAFTLTLAERK
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                NPNKKET1SAQNGAQGQLNGLQVEDLTQETKRSMRLSDDVQGVLVSQVNENSPAEQAGFR
                                                                                                                                                                                                                                                                                                                                                                                      ö
                                                                                                                                                                                                                                                                                                                                                                Length 288;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       241 QGNIITKIEEVEVKSVADFNHALEKYKGKPKRFLVLDLNQGYRIILVK 288
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            QGNIITKIEEVEVKSVADFNHALEKYKGKPKRFLVLDLNQGYRIILVK 387
                                                                                                                                                                                                                                                                                                                                                                                    Indels
                                                                                                                                                                                                                                                                                                                                                               74.4%; Score 288; DB 20; L 100.0%; Pred. No. 6.1e-288; ive 0; Mismatches 0;
                                                                                                                                                                                Claim 16; Page 322-323; 402pp; English.
                                                                                       Fry KE, Lim MY, McAtee CP;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        AAW89977 standard; Protein; 451 AA.
                                                                  (GENE-) GENELABS TECHNOLOGIES INC
                                                                                                                                                         long-lasting immune response
           98WO-US08487
                               97US-0061958
97US-0045107
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Protein encoded by clone b8
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     (first entry)
                                                                                                                                                                                                                                                                                                                                                                         Best Local Similarity 100.
Matches 288; Conservative
                                                                                                            WPI; 1999-009433/01
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Helicobacter pylori
                                                                                                                                                                                                                                                                                                                                         288 AA;
          27-APR-1998;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     18-FEB-1999
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          WO9849314-A2
                                 14-OCT-1997;
                                           25-APR-1997;
                                                                                                                                                                                                                                                                                                                                          Seguence
                                                                                      Chow TP,
                                                                                                                                                                                                                                                                                                                                                                Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               AAW89977;
                                                                                                                                                                                                                                                                                                                                                                                                                                                       160
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   220
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    18.1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          340
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  RESULT 4
a
                                                                                                                                                                                                                                                                                                                                                                                                                                                                          g
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    g
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 g
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ò
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ò
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        셤
                                                                                                                                                                                                                                                                                                                                                                                                                                                        à
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                à
```

```
that is characterised by immunoreactivity with H. pylori-positive antisera. The proteins are highly immunogenic and induce a long-lasting immune response that persists even after antimicriobial treatment. In antibody-detection assays, on sera, plasma, urine, saliva etc., they are highly sensitive and specific. The specification also describes 69 previously unrecognised immunogenic cluster families. H. pylori antigens are used to detect H. pylori-specific antibodies, for diagnosing infection or to confirm eradication of infection, and in vaccines to protect against H. pylori infection and related diseases (gastritis,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            present sequence represents a Helicobacter pylori antigenic protein
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             AVIRITKDNLPTIKFSDSNDISVGDLVFAIGNPFGVGESVTQGIVSALNKSGIGINSYEN 120
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Gaps
                                                                                                                                                                                                                                                                                                                                                                                      New Helicobacter pylori antigens and related nucleic acid sequences - useful in serological diagnosis and protective vaccines, providing long-lasting immune response
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    1 MIPKERMERALGSGVIISKDGYIVTNNHVIDGADKIKVTIPGSNKEYSATLVGTDSESDL 60
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Antigen; immunogenic cluster family; vaccine; gastritis; diagnosis; peptic ulcer; gastric adenocarcinoma; gastric lymphoma.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Length 451;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     FIQTDASINPGNSGGALIDSRGGLVGINTAIISKTGGNHGIGFAI 165
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      42.6%; Score 165; DB 20; 1 100.0%; Pred. No. 5.2e-161;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          peptic ulcer, gastric adenocarcinoma/lymphoma).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Claim 15; Page 317-318; 402pp; English.
                                                                                                                                                                                                                                                    McAtee CP;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Ą.
                                                                                                                                                                                            GENE-) GENELABS FECHNOLOGIES INC.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         42.5,
100.0%; Piv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           AAW89817 standard: Protein; 187
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              S
                                                    98WO-US08487
                                                                                                           97US-0061958
97US-0045107
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            98NO-US08487
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Matches 165; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Protein encoded by clone
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Helicobacter pylogi
                                                                                                                                                                                                                                                                                                        WPI; 1999-009433/01
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Query Match
Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    451 AA;
                                                                                                                                                                                                                                                                                                                                     N-PSDB; AAV90921
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            27-APR-1998;
                                                                                                           14-OCT-1997;
25-APR-1997;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       18-FEB-1999
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           WO9849314-A2
                                                    27-APR-1998;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     05-NOV-1998,
05-NOV-1998
```

ö

```
Claim 12; Page 47-49; 67pp; Japanese.
                                                                                                                                                                                                                                                                                                                                                                                                                          23-MAR-1991;
                                                                                                                                                                                                                                                                                                                                                                                                                                                 30-MAR-1990;
                                                                                                                                                                                                                                                                                                                                                                                WO9115572-A
                                                                                                                                                                                                                                                                                                                                                                                                    17-0CT-1991
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Dougan G,
                                                                                          Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Seguence
                                                                                                                                                                                                                                                          AAR14625;
                                                                                                                Query Match
    õ
                                                                                                                                                                              g
                                                                                                                                                                                                                                                           QQ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         á
                                                                                                                                                                                                                                                                                                                                                          ;
0
                                                                                                                                                                          The present sequence represents a Helicobacter pylori antigenic protein that is characterised by immunoreactivity with H. pylori-positive antisera. The proteins are highly immunogenic and induce a long-lasting immune response that persists even after antimicriobial treatment. In antibody-detection assays, on sera, plasma, urine, saliva etc., they are highly sensitive and specific. The specification also describes 69 previously unrecognised immunogenic cluster families. H. pylori antigens are used to detect H. pylori-specific antibodies, for diagnosing infection or to confirm eradication of infection, and in vaccines to protect against H. pylori infection and related diseases (gastritis, peptic ulcer, gastric adenocarcinoma/lymphoma).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          HtrA; PonA; HypC; YefW; ABC1; Omp100; Lawsonia intracellularis infection;
                                                                                                                                                                                                                                                                                                                                                                             203 YDNKEGAVVISVEKDSPAKKAGILVWDLITEVNGKKVKNTNELRNLIGSMLPNQRVTLKV 262
                                                                                                            New Helicobacter pylori antigens and related nucleic acid sequences - useful in serological diagnosis and protective vaccines, providing
                                                                                                                                                                                                                                                                                                                                                                                          3 YDNKEGAVVISVEKDSPAKKAGILVWDLITEVNGKKVKNTNELRNLIGSMLPNQRVILKV 62
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ដ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Lawsonia intracellularis polynucleotide and encoded protein, used prevent Lawsonia intracellularis infection -
                                                                                                                                                                                                                                                                                                                                                          ;
0
                                                                                                                                                                                                                                                                                                                                   Length 187;
                                                                                                                                                                                                                                                                                                                                                          Indels
                                                                                                                                                                                                                                                                                                                                                                                                                         263 IRDKKERAFTLTLAERKNPNKKETISAQNGAQGQLNGLQVEDLTQ 307
                                                                                                                                                                                                                                                                                                                                                                                                                                      ö
                                                                                                                                                                                                                                                                                                                                  27.1%; Score 105; DB 20;
100.0%; Pred. No. 1.4e-99;
iive 0; Mismatches 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Lawsonia intracellularis protein SEQ ID NO: 7.
                                                        McAtee CP;
                                                                                                                                                       Claim 15; Page 103; 402pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Æ
                                 (GENE-) GENELABS TECHNOLOGIES INC.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   AAG78605 standard; Protein; 474
                                                                                                                                    long-lasting immune response
97US-0061958
97US-0045107
                                                        Lim MY,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            20-OCT-2000; 2000JP-0320736
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  99US-0160922
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               (first entry)
                                                                                                                                                                                                                                                                                                                                             Best Local Similarity 100.
Matches 105; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Lawsonia intracellularis.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      (PFIZ ) PFIZER PROD INC.
                                                                             WPI; 1999-009433/01.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           WPI; 2001-592540/67
                                                        Fry KE,
                                                                                                                                                                                                                                                                                                             187 AA;
                                                                                        N-PSDB; AAV90552
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               JP2001169787-A.
14-OCT-1997;
25-APR-1997;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                22-OCT-1999;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              20-NOV-2001
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     26-JUN-2001
                                                       Chow TP,
                                                                                                                                                                                                                                                                                                               Seguence
                                                                                                                                                                                                                                                                                                                                   Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        AAG78605;
                                                                                                                                                                                                                                                                                                                                                                                                                                              63
                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ESULT 6
AG78605
 à
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              g
                                                                                                                                                                                                                                                                                                                                                                                                                         οy
                                                                                                                                                                                                                                                                                                                                                                                                                                             ద
```

```
ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ö
The present invention provides isolated polynucleotides encoding HtrA, PonA, HypC, LygS, YefW, ABC1 or Omp100 protein of Lawsonla intracellularis. The sequences can be used in vaccines for the prevention of Lawsonia intracellularis infection. The present sequence is a protein of the invention.
                                                                                                                                                                                                                                        Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         TrophoA mutagenesis was used in the mouse virulent S. typhimurium strain C5. Mutants were selected likely to harbour lesions in genes that have a signal peptide sequence, i.e. proteins likely to be targetted through a bacterial membrane. Isolation of the DNA flanking the TrophoA insertion identified the gene (htra) that has been insertionally activated. Comparison of the translated protein sequence showed that it shared 88% homology with the sequence of the
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Chatfield SN;

    attenuated by

                                                                                                                                                                                                                                      ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ö
                                                                                                                                                                                        Length 474;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 mutation in DNA sequence encoding e.g. a heat shock protein
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Length 475;
                                                                                                                                                                                                                                      Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  TnphoA mutagenesis; signal peptide; stress protein;
heat shock protein; degP.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Hormaeche CE, Johnson KS,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  DB 12; Lv
0.0024;
thes 0;
                                                                                                                                                                                        DB 22; L
                                                                                                                                                                                                                                          ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Attenuated microorganism useful in live vaccines
                                                                                                                                                                                        3.4%; Score 13; DB 100.0%; Pred. No. 0.C
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Score 12;
Pred. No.
                                                                                                                                                                                                                                                                                                                                                                                                                                                 AAR14625 standard; Protein; 475 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Disclosure; Fig 1; 28pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Salmonella typhimurium strain C5
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            (WELL ) WELLCOME FOUNDATION LTD.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  3.1%; Sconstity 100.0%; Procervative 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                91WO-GB00484.

 typhimurium HtrA protein.

                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              90GB-0007194
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           14-JAN-1992 (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           htra product from E. coli
                                                                                                                                                                                                                                        Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Charles IG,
                                                                                                                                                                                                                                                                                    123 QTDASINPGNSGG 135
                                                                                                                                                                                                                                                                                                                                  219
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            160 GIGFAIPSNMVK 171
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      11111111111
264 GIGFAIPSNMVK 275
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   WPI; 1991-325215/44.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Query Match
Best Local Similarity
Matches 12; Conserv
                                                                                                                                                                                                                Best Local Similarity
Matches 13; Conserv
                                                                                                                                                                                                                                                                                                              207 QTDASINPGNSGG
                                                                                                                                            474 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       475 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              N-PSDB; AAQ14416.
```

RESULT 8
AAW56771

```
The invention relates to isolated polynucleotide (I) and polypeptide (II) sequences. (I) is useful as hybridisation probes, polymerase chain seaction (PGR) primers, oligomers, and for chromosome and gene mapping, and in recombinant production of (II). The carbon of control of the control of
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Streptococcus; GAS; GBS; group B streptococcus; Streptococcus agalactiae; group A streptococcus; Streptococcus pyogenes; antibacterial; antiinflammatory; infection; vaccine; meningitis; gene therapy.
                                                                                                                                                                                                                                                                                               New isolated polynucleotide and encoded polypeptides, useful in diagnostics, forensics, gene mapping, identification of mutations responsible for genetic disorders or other traits and to assess biodiversity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             2.8%; Score 11; DB 22; Length 168; 100.0%; Pred. No. 0.0091; rive 0; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            at ftp.wipo.int/pub/published_pct_sequences
                                                                                                                                                                                                                                                                                                                                                                                                                                  Claim 20; SEQ ID No 55622; 103pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Streptococcus polypeptide SEQ ID NO 5102.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ABP27963 standard; Protein; 380 AA.
                                                                                                                                                                             Tang YT;
30-MAR-2001; 2001WO-US08631.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  29-OCT-2001; 2001WO-GB04789
                                                  2000US-0540217
2000US-0649167
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         02-JUL-2002 (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Best Local Similarity 100.
Matches 11; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Streptococcus agalactiae.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    100 ENFIQTDASIN 1.10
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    119 ENFIQTDASIN 1.29
                                                                                                                                                                             Drmanac RT, Liu C,
                                                                                                                                                                                                                        WPI; 2001-639362/73.
N-PSDB; AAS89450.
                                                                                                                         (HYSE-) HYSEQ INC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              WO200234771-A2.
                                                  31-MAR-2000;
23-AUG-2000;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                02-MAY-2002.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                RESULT 10
ABP27963
  ò
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Gaps
                                                                                                                                                                                                                                                                          PS-1; presentlin; presentlin-1; PSP-1; Alzheimer's disease; htrA; serine protease; neurodegeneration; predisposition; diagnosis.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Nucleic acids encoding human serum protease protein(s) – used for diagnosing pre-disposition to Alzheimer's disease, etc.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Human; chromosome mapping; gene mapping; gene therapy; forensic; food supplement; medical imaging; diagnostic; genetic disorder.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      The sequence is that of the serine protease htrA which was used in the isolation of \mathsf{PSP1}.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ó
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Query Match 3.1%; Score 12; DB 19; Length 491; Best Local Similarity 100.0%; Pred. No. 0.0025; Matches 12; Conservative 0; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    , Clinkenbeard HE, Creasy CL, Karran EH; Southan CD;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Novel human diagnostic protein #25254.
                                                                                                                                                                                                                          Escherichia coli serine protease htrA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Example 2; Page 28-29; 65pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ABG25263 standard; Protein; 168 AA.
                                                                       AAW56771 standard; Protein; 491 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             (SMIK ) SMITHKLINE BEECHAM CORP.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         96US-0032875.
96US-0025436.
96US-0027873.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          97EP-0306501.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      18-FEB-2002 (first entry)
                                                                                                                                                                           (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 11111111111
263 GIGFAIPSNMVK 274
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    160 GIGFAIPSNMVK 171
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 WPI; 1998-161101/15.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Sequence 491 AA;
                                                                                                                                                                                                                                                                                                                                                      Escherichia coli.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           N-PSDB; AAV29528
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   WO200175067-A2.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         13-DEC-1996;
06-SEP-1996;
25-OCT-1996;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          26-AUG-1997;
                                                                                                                                                                        13-OCT-1998
                                                                                                                                                                                                                                                                                                                                                                                                     EP828003-A2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        11-0CT-2001
                                                                                                                                                                                                                                                                                                                                                                                                                                                       11-MAR-1998
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Browne MJ,
Livi GP, S
                                                                                                                         AAW56771;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ABG25263;
```

RESULT 9

ò

ö

Gaps

```
WO200039309-A1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Bolotine A,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     RESULT 12
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ABB55490
     g
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             å
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ö
                                                                                                                                                                                                                                                                                                                                                                                       streptococcus/GBS (Streptococcus agalactiae) or group, A streptococcus/GBS (Streptococcus agalactiae) or group, A streptococcus/GBS (Streptococcus pyogenes), comprising one of 5483 sequences (51), given in the specification. The proteins have antibacterial and antiinflammatory activity. (1), nucleic acids encoding (1), ABMSG044-ABM71526 and antibodies that bind (1) are used in the manufacture of medicaments for the treatment or prevention of infection or disease caused by streptococcus bacteria, particularly S. agalactiae and S. pyrogenes. Nucleic acids encoding (1) are used to detect Streptococcus in a biological sample. (1) is used to detecmine whether a compound binds to (1). A composition composition or disease caused by the disease caused by the composition or disease caused by the composition or disease caused by the composition or disease caused by the caused as a vaccine or disease caused by the composition or disease caused by the caused as a caused as a vaccine or disease caused by the caused as a vaccine or disease caused by the caused as a caused as a vaccine or disease caused by the caused as a vaccine or disease caused by the caused as a vaccine or disease caused by the caused as a vaccine or disease caused by the caused as a vaccine or disease caused by the caused as a cause or determine whether a composition caused as a vaccine or disease caused by the caused caused by the cause of t
                                                                                                                                                                                                                                                          New Streptococcus protein for the treatment or prevention of infection or disease caused by Streptococcus bacteria, such as meningitis, and for detecting a compound that binds to the protein -
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Streptococcus that is prevented or treated may be meningitis. Nucleic acid encoding (I) may be used to recombinantly produce (I) and may be used in gene therapy. Antibodies to (I) are used for affinity chromatography, immunoassays, and distinguishing/identifying
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Catalytic site; protease; HtrA; surface protease; fermented product; vaccine; dietary protein; cheese production; digestive enzyme.
                                                                                                                                                                                                                                                                                                                                                                         The invention relates to a protein (ABP25413-ABP30895) from group B
                                                                                                                                                   Grandi G, Fraser C;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                2.8%; Score 11; DB 23; Length 380;
100.0%; Pred. No. 0.021;
ive 0; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     The HtrA surface protease of Lactococcus lactis.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         /note= "transmembrane domain"
119..129
                                                                                                                                                   Masignani V, Margarit Ros YI,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            'note= "catalytic domain"
157..164
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       /note= "catalytic domain"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   "catalytic domain"
                                                                                                                                                                                                                                                                                                                                      Claim 1; Page 3673; 4525pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         AAY93768 standard; Protein; 408 AA.
                 27-OCT-2000; 2000GB-0026333.
24-NOV-2000; 2000GB-0028727.
07-MAR-2001; 2001GB-0005640.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    /note= "c
237..254
                                                                                         (CHIR-) CHIRON SPA.
(GENO-) INST GENOMIC RES.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         11; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Streptococcus proteins
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          128 INPGNSGGALI 138
                                                                                                                                                                                                      WPI; 2002-352536/38.
N-PSDB; ABN68594.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  103 INPGNSGGALI 213
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Best Local Similarity
Matches 11; Conserva
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     actococcus lactis.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               380 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            )isulfide-bond
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 03-OCT-2000
                                                                                                                                                 Telford J,
Tettelin H;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              AAY93768;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Domain
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Domain
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Domain
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      RESULT 11
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     AAY93768
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             g
\mathbb{Z}_{\times}^{\times}
```

```
The present sequence represents a HtrA surface antigen from Lactococcus lactis subsp. lactis. The specification describes a method for the production of a protein. The method comprises culturing a bacterial strain that expresses the protein and is prepared from a Gram-positive species with a genome no larger than 3.2 Mb by mutational inactivation of the HtrA surface protease, and recovering the protein exported from the cells. Inactivation of HtrA almost completely eliminates degradation of exported proteins, so increases yields of the protein and prevents contamination by proteolytic degradation products (facilitating purification at reduced cost). The bacterial strain is used for preparation of fermented products, therapeutic proteins (especially vaccines) or dietary proteins (e.g. for the production of cheeses or enzymes for facilitating digestion).
                                                                                                                                                                                                                                                                                                                                                                                                                                                   Bacteria deficient in activity of protease HtrA, useful for production of proteins, e.g. vaccinating antigens, that are exported from the cell, provide increased yield
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Biosynthesis; biodegradation; lactic bacterium; yogurt; cheese.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              2.8%; Score 11; DB 21; Length 408; 100.0%; Pred. No. 0.022; Ure 0; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Sorokine A, Renault P, Ehrlich SD;
                                                                                                                                                                                                                                                                                  Poquet I, Gruss A, Bolotine A, Sorokine A;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            (INRG ) INRA INST NAT RECH AGRONOMIQUE.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ABB55490 standard; Protein; 408 AA.
                                                                                                                                                                                                         (INRG ) INST NAT RECH AGRONOMIQUE.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Disclosure; Fig 1; 42pp; French.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Lactococcus lactis protein htra.
                                                                                                                                       98FR-0016462.
                                                                 99WO-FR03270
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      11-APR-2000; 2000FR-0004630.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                11-APR-2000; 2000FR-0004630
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      16-MAY-2002 (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Best Local Similarity 100. Matches 11; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Lactococcus lactis IL1403
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 128 INPGNSGGALI 138
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         234 INPGNSGGALI 244
                                                                                                                                                                                                                                                                                                                                                    WPI; 2000-465747/40.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    408 AA;
                                                                                                                                                                                                                                                                                                                                                                                         N-PSDB; AAA47161
                                                                     23-DEC-1999;
                                                                                                                                       24 - DEC - 1998;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         FR2807446-A1.
06-JUL-2000
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           12-OCT-2001
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ABB55490;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Query Match
```

ö

us-09-895-913a-120_1.rag

```
and for screening secreted antigens
                                                                                                                                                                                                                                                                                                                                                                      WO200234771-A2.
                                                                                                                                                                                                                                                  02-JUL-2002
                                                                                                                                                                                                                                                                                                                                                                                              02-MAY-2002.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Pettelin H;
                                                                                                                                                                                                                           ABP29849;
                                                 Sequence
                                                                                                                                                                             RESULT 14
ABP29849
 SSSSXS
                                                                                                                     ò
                                                                                                                                          g
                                                                                                                                                                                                                ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      AAA05803 to AAA05872 encode proteins, polypeptides and peptides (given in AAY91275 to AAY91343) isolated from Group B Streptococcus (GBS), also Mown as Streptococcus agalactiae. The GBS polynucleotides and polypeptides have antibacterial activity. Immunopenic compositions comprising GBS polynucleotides or polypeptides can be used as vaccines and for the treatment or prophylaxis of GBS infection. The polynucleotides and polypeptides can also be used in the detection of GBS
                                                                           The present invention is related to a Lactococcus lactis nucleotide sequence (ABA9021) and related proteins (ABB53300-ABB55621). The nucleic acid sequence; is useful in the detection and/or amplification of nucleic acid sequence, particularly to identify Lactococcus lactis or related species. The proteins of the invention are useful for the biosynthesis or biodegradation of a composition of interest. The invention helps research in lactic bacteria, particularly useful in the production of yogurt and cheese.

Note: The sequence data for this patent is based on equivalent patent wo200177334 (published 18-Ocr-2001) which is available in electronic format directly from WIPO at ftp.WiPo.int/pub/published_pct_sequences.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              New Group B Streptococcus protein, useful as vaccine, for diagnosis of Streptococcal infections and for screening of antibodies or affibodies
                                                                                                                                                                                                                                                                          Gaps
                       sequence useful in the identification or Lactococcus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Group B Streptococcus; Streptococcus agalactiae; protein antigen; vaccine; screening; immunogen; detection; diagnosis; infection; antibody; affibody; antibacterial.
                                                                                                                                                                                                                                                                          ;
                                                                                                                                                                                                                                                2.8%; Score 11; DB 23; Length 408;
100.0%; Pred. No. 0.022;
                                                                                                                                                                                                                                                                          0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                     Group B Streptococcus protein sequence SEQ ID NO:67.
                                                                                                                                                                                                                                                       100.0%; Preu. ...
                                                        Claim 6; SEQ ID No 2192; 2504pp; French.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Hanniffy SB;
                                                                                                                                                                                                                                                                                                                                                                                AAY91334 standard; Protein; 409 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Claim 1; Fig 1; 123pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         (MICR-) MICROBIAL TECHNICS LTD
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 99WO-GB02444.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      98GB-0016335,
99US-0125163,
                                   lactis and related species
                                                                                                                                                                                                                                                                                                                                                                                                                              (first entry)
                                                                                                                                                                                                                                                                         11; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Streptococcus agalactiae
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Le Page RWF, Wells JM,
                                                                                                                                                                                                                                                                                                128 INPGNSGGALI 138
                                                                                                                                                                                                                                                                                                            WPI; 2000-195299/17.
WPI; 2002-043418/06
                                                                                                                                                                                                                                                           Best Local Similarity
                                                                                                                                                                                                                           408 AA;
                       New nucleotide
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  WO200006736-A2.
                                                                                                                                                                                                                                                                                                                                                                                                                              30-MAY-2000
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               27-JUL-1999;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       27-JUL-1998;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  19-MAR-1999;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         10-FEB-2000
                                                                                                                                                                                                                           Sequence
                                                                                                                                                                                                                                                                                                                                                                                                        AAY91334;
                                                                                                                                                                                                                                                  Query Match
                                                                                                                                                                                                                                                                         Matches
                                                                                                                                                                                                                                                                                                                                                         RESULT 13
                                                                                                                                                                                                                                                                                                                                                                    AAY91334
                                                                                                                                                                                                                                                                                                                      쉽
```

```
The invention relates to a protein (ABP25413-ABP30895) from group B streptococcus/GBS (Streptococcus agalactiae) or group A streptococcus/GBS (Streptococcus agalactiae) or group A streptococcus/GBS (Streptococcus sydgences (S1), given in the specification. The proteins have antibacterial and antiinflammatory cativity. (I), nucleic acids encoding (I), ABN66044-ABN71526 and attibodies that bind (I) are used in the manufacture of medicaments for the treatment or prevention of infection or disease caused by Streptococcus bacteria, particularly S. agalactiae and S. pyrogenes. Nucleic acids encoding (I) are used to detect Streptococcus in a compound binds to biological sample. (I) is used to detect Streptococcus in a composition comprising (I) or a nucleic acid encoding (I), may be composition avaccine or diagnostic composition. The disease caused by Streptococcus that is prevented or treated may be meningitis. Nucleic acid encoding (I) may be used to recombinantly produce (I) and may be used in gene therappy. Antibodies to (I) are used for affainty chromatography, immunoassays, and distinguishing/identifying
                                                                                                                                                                                                                                                                                                                                    ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Streptococcus; GAS; GBS; group B streptococcus; Streptococcus agalactiae; group A streptococcus; Streptococcus pyogenes; antibacterial; antiinflammatory; infection; vaccine; meningitis; gene therapy.
                                      secreted antigens in gram positive bacteria. AAA05873 to AAA05941 represent primers used in the exemplification of the present invention
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                New Streptococcus protein for the treatment or prevention of infection or disease caused by Streptococcus bacteria, such as meningitis, and for detecting a compound that binds to the protein -
                                                                                                                                                                                                                                                                                                                                    Gaps
DNA encoding bacterial cell envelope associated or
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Telford J, Masignani V, Margarit Ros YI, Grandi G, Fraser C;
                                                                                                                                                                                                                                                                                                                                    ;
0
                                                                                                                                                                                                                                                  2.8%; Score 11; DB 21; Length 409; 100.0%; Pred. No. 0.022; ive 0; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Streptococcus polypeptide SEQ ID NO 8874.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Claim 1; Page 4005; 4525pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ABP29849 standard; Protein; 409 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    27-OCT-2000; 2000GB-0026333.
24-NOV-2000; 2000GB-0028727.
07-MAR-2001; 2001GB-0005640.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           29-OCT-2001; 2001WO-GB04789
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                (first entry)
                                                                                                                                                                                                                                     Query Match 2.8 Best Local Similarity 100. Matches 11, Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    (GENO-) INST GENONIC RES.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Streptococcus agalactiae
                                                                                                                                                                                                                                                                                                                                                                                                                                                                 232 INPGNSGGALI 342
                                                                                                                                                                                                                                                                                                                                                                                                                      128 INPGNSGGALI 1.38
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           WPI; 2002-352536/38.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             (CHIR-) CHIRON SPA.
                                                                                                                                                                409 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          N-PSDB; ABN70480
```

ö

```
á
                                                                                      qq
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Streptococcus/GBS (Streptococcus agalactiae) or group A streptococcus/GAS (Streptococcus pyogenes), comprising one of 5483 sequences (51), given in the specification. The proteins have antibocterial and antihiflammatory activity. (1), nucleic acids encoding (1), ABMS6044-ABM71526 and antibodies that bind (1) are used in the manufacture of medicaments for the treatment or prevention of infection or disease caused by Streptococcus bacteria, particularly S. agalactiae and S. pyrogenes. Nucleic acids encoding (1) are used to detect Streptococcus in a composition comprising (1) or a nucleic acid encoding (1); may be used as a vaccine or diagnostic composition. The disease caused by Streptococcus that is prevented or treated may be meningitis. Nucleic acid encoding (1) may be used to recombinantly produce (1) and may be used in gene therapy. Antibodies to (1) are used for affinity chromosomy, immunoassays, and distinguishing/identifying
                                                                    ö
                                                                                                                                                                                                                                                                                                                                                                Streptococcus; GAS; GBS; group B streptococcus; Streptococcus agalactiae; group A streptococcus; Streptococcus pyogenes; antibacterial; antilnflammatory; infection; vaccine; meningitis; gene therapy.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       New Streptococcus protein for the treatment or prevention of infection or disease caused by Streptococcus bacteria, such as meningitis, and for detecting a compound that binds to the protein -
                                                                      Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              The invention relates to a protein (ABP25413-ABP30895) from group B
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Grandi G, Fraser C;
                                                                      ö
                                2.8%; Score 11; DB 23; Length 409; 100.0%; Pred. No. 0.022; Live 0; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Margarit Ros YI,
                                                                                                                                                                                                                                                                                                                                   Streptococcus polypeptide SEQ ID NO 9446.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Claim 1; Page 4070; 4525pp; English.
                                                                                                                                                                                                                            ABP30135 standard; Protein; 409 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          27-OCT-2000; 2000GB-0026333.
24-NOV-2000; 2000GB-0028727.
07-MAR-2001; 2001GB-0005640.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          29-OCT-2001; 2001WO-GB04789
                                                                                                                                                                                                                                                                                               (first entry)
                                                  Best_Local Similarity 100.
Matches 11; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 (CHIR-) CHIRON SPA. (GENO-) INST GENOMIC RES.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Masignani V,
                                                                                                                                                                                                                                                                                                                                                                                                                                        Streptococcus agalactiae
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Streptococcus proteins.
                                                                                                     128 INPGNSGGALI 138
                                                                                                                          232 INPGNSGGALI 242
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   WPI; 2002-352536/38.
409 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                409 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      N-PSDB; ABN70766
                                                                                                                                                                                                                                                                                                                                                                                                                                                                       WO200234771-A2.
                                                                                                                                                                                                                                                                                               02-JUL-2002
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           02-MAY-2002.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Telford J,
Tettelin H;
Sequence
                                                                                                                                                                                                                                                             ABP30135;
                                  Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Sequence
                                                                                                                                                                                        RESULT 15
ABP30135
                                                                                                     ŏ
                                                                                                                                     8
```

```
Query Match
2.8%; Score 11; DB 23; Length 409;
Best Local Similarity 100.0%; Pred. No. 0.022;
Matches 11; Conservative 0; Mismatches 0; Indels 0; Gaps
Qy 128 INPGNSGGALI 138
Db 232 INPGNSGGALI 242
Search Completed: November 18, 2002, 11:34:26
Job time: 42 secs
```

```
sec,
                                                                                                               November 18, 2002, 11:33:16; Search time 13 Seconds (without alignments)
GenCore version 5.1.3 Copyright (c) 1993 - 2002 Compugen Ltd.
                                                                              OM protein - protein search, using sw model
                                                                                                                     Run on:
```

	1234.718 Million cell updates/s
Title: Perfect score:	US-09-895-913A-120 387
Sequence:	1 MIPKERMERALGSGVIISKDRPKRFLVLDLNQGYRIILVK 387
Scoring table: OLIGO Gapop	OLIGO Gapop 60.0 , Gapext 60.0
Searched:	112892 segs, 41476328 residues
Word size :	0

Minimum DB seq length: 0 Maximum DB seq length: 200000000

Total number of hits satisfying chosen parameters:

112892

Post-processing: Listing first 45 summaries

SwissProt_40:* Database :

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

	Description	P45129 haemophilus	'n		6 lactococcu	_	P54925 bartonella .	P44947 haemophilus		lactobaci	-	arabidopsi			buchnera	rickettsi	005942 rickettsia	Q92912 bacillus ha	Q06927 pepper huas	tomato	bombyx	Q96us8 sclerotinia	Q9lu10 arabidopsis		_	P18584 chlamydia t	047427 branchiosto	O21003 branchiosto	Q9z9k6 bacillus ha	O69232 buchnera ap	Q04120 saccharomyc		7268	P45289 haemophilus
SUMMARIES	CI CI	HTOA_HAEIN	DEGP_ECOLI	DEGP_SALTY	HTRA_LACLA	DEGO_ECOLI	DEGP_BARHE	DEGS_HAEIN	YYXA_BACSU	HTRA_LACHE	DEGP_CHLPN	DEG1_ARATH	HTRA_BACSU	DEGP_BUCAI	DEGP_BUCAP	DEGP_RICCN	DEGP_RICPR	RL23_BACHD	VBR1_PHUV	VBR1_TGMV	RL5_BOMMO	G3P_SCLSC	DEG8_ARATH	- 1	- 1	DEGP_CHLTR	ATP8_BRAFL	ATP8_BRALA	RL29_BACHD	RPOA_BUCAP	TSA2_YEAST	ď	VBR1_PYMVV	SAPF_HAEIN
	DB	н	-	Н	1	-	Н	Н	Н	Н	-	-	-	Н	Н	~	Н	-	-	-	Н	7	7	7	-	-	-			Н	7	7	-	7
	Length	466	474	475	408	455	503	340	400	413	488	437	449	478	478	508	513	96	256	256	299	338	448	458	497	497	54	54	29	113	195	221	256	269
æ	Query		3.1	•		٠			5.6					٠				2.1	٠	2.1						2.1	٠	1.8	•	٠	1.8	٠	1.8	1.8
•	Score	12	12	12	11	11	11	10	10	10	10	σ	σ	σ	σ	6	6	80	6 0	80	œ	œ	80	œ	Φ.	œ	7	7	7	7	7	7	7	7
	Result No.	1	7	m	4	Ŋ	ø	7	80	σ	10	11	12	13	14	15	16	17	18	19	20	21	22	23	24	25	56	27	28	29	30	31	35	33

P54382 bacillus su P96050 streptococc P52839 arabidopsis Q15612 homo sapien O78702 manis tetra O78702 manis tetra P43737 haemophilus P005744 escherichia P57941 pasteurella Q82587 yersinia pe Q37556 metridium s Q00584 claviceps p		HARIA HEROA HERIN HARIA HARIA HARIA HARIA HARIA HARIA HARIA HATOA, HARIA	oeat; Signal;
.8 283 1 FOLD_BACSU .8 284 1 FOLD_STRTR .8 302 1 FSTL_ARATH .8 314 1 NOIM_LHUMAN .8 318 1 NOIM_LANCA .8 329 1 RPOM_HAEIN .8 329 1 RPOM_PASHU .8 337 1 G3P_CLAPU	ALIGNMENTS	FEULT 1 TOA HAETH TOA HAETH TOA HAETH TO 10 NOV-1995 (Rel. 32, Created) 15-0100-1000-1995 (Rel. 32, Last sequence update) 15-010-1000-1995 (Rel. 32, Last sequence update) 16-010-1000-1995 (Rel. 32, Last sequence update) 17-010-1995 (Rel. 20, Mams M. D., White O., Clayton R. A., Kelley J. M., Merland J. C., Phillips C.A., Spriggs T., Heddlom E., Cotton M. D., Wetchand J. C., Phillips C.A., Spriggs T., Heddlom E., Cotton M. D., Utterback T. R., Hand M. C., Nayapa D. T., Saudle D. M., Smith H. O., Otter J. C., McConald L. A., Small K. V., Fraser C. M., Smith H. O., Otter J. C., McConald L. A., Small K. V., Fraser C. M., Smith H. O., Otter J. C., McConald L. A., Small K. V., Fraser C. M., Smith H. O., Otter J. C., McConald L. A., Small K. V., Fraser C. M., Smith H. O., Otter J. C., McConald L. A., Small K. V., Fraser C. M., Smith H. O., Otter J. C., McConald L. A., Small K. V., Fraser C. M., Smith H. O., Otter J. C., McConald L. A., Small K. V., Fraser C. M., Smith H. O., Otter J. C., McConald L. A., Small K. V., Fraser C. M., Smith H. O., Otter J. C., McConald L. A., Small K. V., Fraser C. M., Smith H. O., Otter J. C., McConald L. J. C., Smith H. O., Otter J. C., McConald L. J. C., State J. C., McConald L. J. C., Smith H.	ine protease; Periplasmic; Repeat;
335 335 336 337 441 441 454 454 454 454 454 454 454 454		HTOA_HAEIN HTOA_HAEIN HTOA_HAEIN HTOA_HAEIN HTOA_HAEIN HTOA_HAEIN DT 01-NOV-1995 (Rel. 32, Lass) DE 15-JUN-2002 (Rel. 11, Lass) DE 15-JUN-2002 (Rel. 11, Lass) DE 15-JUN-2002 (Rel. 11, Lass) DE 16-JUN-21	Hydrolase; Serine
		A H H H H S O O O O O O O O O O O O O O O	KW

```
EMBL;
EMBL;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            EMBL;
EMBL;
  ;
0
                                                                                                                                     Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                MEDLINE-97426617; PubMed-9278503;
MEDLINE-97426617; PubMed-9278503;
Blattner F.R., Plunkett G. III, Bloch C.A., Perna N.T., Burland V.,
Riley M., Collado-Vides J., Glasner J.D., Rode C.R., Mayhew G.F.,
Gregor J., Davis N.W., Kirkpatrick H.A., Goeden M.A., Rose D.J.,
Mau B., Shao Y.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Fujita N., Mori H., Yura T., Ishihama A.; Systematic sequencing of the Escherichia coli genome: analysis of the 2.4 4.1 min (110, 917-193, 643 bp) region."; Nucleic Acids Res. 22:1637-1639(1994).
                    PROBABLE PERIPLASMIC SERINE PROTEASE
                                                                                                                                                                                                                                                                                                                                                                                               Lipinska B., Sharma S., Georgopoulos C.; "Sequence analysis and regulation of the htrA gene of Escherichia coli: a sigma 32-independent mechanism of heat-inducible
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   SEQUENCE FROM N.A.
Schramm S., Duncan M., Allen E., Araujo R., Aparicio A., Chung E.
Davis K., Federspiel N., Hyman R., Kalman S., Komp C., Kurdi O.,
Lashkari D., Lew H., Lin D., Namath A., Oefner P., Roberts D.,
                                                                                                                                                                                                                                                                                                                           Proteobacteria; gamma subdivision; Enterobacteriaceae;
                                                                                                                                     .
0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         SEQUENCE FROM N.A.
STRAIN=0157:H7 / EDL933 / ATCC 700927;
MEDLINE=21074935; Pubmed=11206551;
Perna N.T., Plunkett G. III, Burland V., Mau B., Glasner J.D.,
                                                           CHARGE RELAY SYSTEM (POTENTIAL).
CHARGE RELAY SYSTEM (POTENTIAL).
CHARGE RELAY SYSTEM (POTENTIAL).
                                                                                                               3.1%; Score 12; DB 1; Length 466; 100.0%; Pred. No. 0.00023; .ive 0; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     "The complete genome sequence of Escherichia coli K-12."; Science 277:1453-1474(1997).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Submitted (SEP-1996) to the EMBL/GenBank/DDBJ databases
                                                                                            ED050A00047B5851 CRC64;
                                                                                                                                                                                                                           DEGREECOLI STANDARD, PRT; 474 AA.
P09376; P15724;
01-MAR-1999 (Rel. 10, Created)
15-JUN-2002 (Rel. 41, Last sequence update)
15-JUN-2002 (Rel. 41, Last annotation update)
15-JUN-2002 (Rel. 41, Last annotation update)
DEGREE OF HITRA-OR-PITO OR B0161 OR 20173 OR ECS0165.
PSCHEFICHIA COLL, and
Bacherichia coll, and
                              DO/HHOA-LIKE.
                                                                                                                                                                                                                                                                                                                                                                                                                                        Nucleic Acids Res. 16:10053-10067(1988)
                                                                                                                                                                                                                                                                                                                                                                           STRAIN-K12;
MEDLINE-89057448; PubMed=3057437;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                      STRAIN-K12 / W3110;
MEDLINE-94261430; Pubmed-8202364;
                                                                                          49434 MW;
                                                                                                                        Local Similaricy hes 12; Conservative
                                                                                                                                                                                                                                                                                                                                             NCBI_TaxID=562, 83334;
                                                                                                                                                                   117 TNNHVIDGADKI 128
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    [3]
SEQUENCE FROM N.A.
STRAIN-KI2 / MG1655;
                                                                                                                                                        TNNHVIDGADKI 36
                                      270
367
120
150
226
466 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                          SEQUENCE FROM N.A. STRAIN-K12 / W3110;
Complete proteome. SIGNAL 1
                                                                                                                                                                                                                                                                                                                                                                   SEQUENCE FROM N.A.
                    30
                                                                                                                                                                                                                                                                                                                                                                                                                               transcription.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Davis R.W.;
                                                                                                                                                                                                                                                                                                                                      Escherichia
                                                           ACT_SITE
ACT_SITE
ACT_SITE
SEQUENCE
                                                                                                                                                                                                                                                                                                                           Bacterta;
                                                                                                              Query Match
Best Local 9
                                                  DOMAIN
                                         DOMAIN
                    CHAIN
                                                                                                                                   Matches
                                                                                                                                                                                                                   DEGP_ECOLI
                                                                                                                                                        25
                                                                                                                                                                                                           RESULT
                                                                                                                                                                                                                                         WHITH THE SO
                                                                                                                                                        ò
                                                                                                                                                                           g
```

```
This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/
                                                                                                                                                                                                                                                                                   STRAIN-015:H7 / RIMD 0509952;
STRAIN-015:H7 / RIMD 0509952;
MEDLINE-21156231; PubMed-11258796;
Hayashi T., Makino K., Ohnishi M., Kurokawa K., Ishii K., Yokoyama K., Han C.-G., Ohtsubo E., Nakayama K., Murata T., Tanaka M., Tobe T., Iida T., Takami H., Honda T., Sasakawa C., Ogasawara N., Yasunaga T., Kuhara S., Shiba T., Hattori M., Shinagawa H.; "Complete genome sequence of enterohemorrhagic Escherichia coli (Complete genomic comparison with a laboratory strain K-12.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Lipinska B., Zylicz M., Georgopoulos C.; "The HtrA (DegP) protein, essential for Escherichia coli survival at high temperatures, is an endopeptidase."; J. Bacteriol. 172:1791-1797(1990).
Rose D.J., Mayhew G.F., Evans P.S., Gregor J., Kirkpatrick H.A., Posfai G., Hackett J., Klink S., Boutin A., Shao Y., Miller L., Grobbeck E.J., Davis N.W., Lim A., Dimalanta E.T., Potamousis K., Apodaca J., Anantharaman T.S., Lin J., Yen G., Schwartz D.C., Welch R.A., Blattner F.R.; "Genome sequence of enterchaemorrhagic Escherichia coli O157:H7."; Nature 409:529-533(2001).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             MEDIINE-90207273; PubMed-2157212;
Wurgler S.M., Richardson C.C.;
"Structure and regulation of the gene for dGTP triphosphohydrolase
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               -i- INDUCTION: BY HEAT SHOCK.
-i- MISCELLANEOUS: HTRA IS INDISPENSABLE FOR BACTERIAL SURVIVAL AT TEMPERATURES ABOVE 42 DEGREES CELSIUS.
-i- SIMILARITY: BELONGS TO PEPTIDASE FAMILY S2C.
-i- SIMILARITY: CONTAINS 2 PDZ/DHR DOMAINS.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Quirk S., Bhatnagar S.K., Bessman M.J.; "Primary structure of the deoxyguanosine triphosphate triphosphohydrolase-encoding gene (dgt) of Escherichia coll.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Proc. Natl. Acad. Sci. U.S.A. 87:2740-2744(1990).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  CHARACTERIZATION, AND SEQUENCE OF 27-39
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  MEDLINE=90323597; PubMed=2165018;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              MEDLINE-90202693; PubMed-2180903;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            MEDLINE-9122240; PubMed-2025286;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        IDENTITY OF HTRA AND PROTEASE DO
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    x12457; CAA30997.1; -. D26562; BAA05608.1; -. AE000125; AAC73272.1; -. U70214; AAG8591.1; -. AE005192; AAG54465.1; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       EMBL; M36536; AAA23994.1; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    SEQUENCE OF 1-50 FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       SEQUENCE OF 1-16 FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  DNA Res. 8:11-22(2001).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   from Escherichia coli.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Gene 89:13-18(1990).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         STRAIN=K12;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       10]
```

ᠬ

```
This SWISS-PROT entry is copyright. It is produced through a cyllaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the Buropean Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Lactococcus lactis (subsp. lactis) (Streptococcus lactis).
Bacteria; Firmicutes; Lactobacillales; Streptococcaceae; Lactococcus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 PROSITE; PS50106; PDZ; 2.
Hydrolase; Serine protease; Heat shock; Periplasmic; Repeat; Signal;
                 Nature 413:852-856(2001).

-!-PUICALON:-SERRINE-PROTEASE-THAT-FS-REQUIRED AT HIGH TEMPERATURE.
-!-FUICALON:-SERRINE-PROTEASE-THAT-FS-REQUIRED AT HIGH TEMPERATURE.
-!-INVOLVED IN THE DEGRADATION OF DAMAGED PROFELINS. SHARED SPECIFICITY WITH HHAD/DEGO.
-!-SUBCELLULAR LACATION: Periplasmic.
-!-INDUCTION: BY HEAT SHOCK.
-!-SIMILARITY: BILONGS TO PEPTIASE FAMILY S2C.
-!-SIMILARITY: CUNTAINS 2 PDZ/DHR DOMAINS.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        STRAIN=IL1403; STRAIN=IL1403; STRAIN=IL1403; STRAIN=IL1403; STRAIN=IL1403; STRAIN=IL1403; STRAIN=IL1601712686; POPQUEL I., Saint V., Seznec E., Simoes N., Bolotin A., Gruss A.; "Htra is the unique surface housekeeping protease in Lactococcus lacits and is required for natural protein processing."; Mol. Microbiol. 35:1042-1051(2000).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          CHARGE RELAY SYSTEM (POTENTIAL).
CHARGE RELAY SYSTEM (POTENTIAL).
CHARGE RELAY SYSTEM (POTENTIAL).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Length 475;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      86E685BF3C1A289F CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         16-OCT-2001 (Rel. 40, Created)
16-OCT-2001 (Rel. 40, Last sequence update)
15-JUN-2002 (Rel. 41, Last annotation update)
15-June protease dc-like htra (EC 3.4.21.-) (Htrall).
HTRA OR LL2136.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       3.1%; Score 12; DB 1; Le
100.0%; Pred. No. 0.00024;
ive 0; Mismatches 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 408 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       BY SIMILARITY. PROTEASE DO.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       [1] SEQUENCE FROM N.A., AND CHARACTERIZATION.
                                                                                                                                                                                                                                                                                                                                                                                                                                        InterPro; IPR001478; PD2.
InterPro; IPR001940; PD2.
InterPro; IPR001244; Ser_protease_C.
InterPro; IPR0012144; Ser_protease_Try.
Pfam; PF00089; trypsin; 1.
Pfam; PF00595; PD5; 2.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                PRT;
                                                                                                                                                                                                                                                                                                                                  EMBL; X54548; CAA38420.1; -. EMBL; AE008704; AAL19173.1; -. EMBL; S15337; S15337. PIR; S21327. S21347. MEROPS; S01.273; degp.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      49315 MW;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            PRINTS; PR00834; FROTEASES2C
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Local Similarity 100.
nes 12; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 STANDARD;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       26
475
372
467
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     1111111111
264 GIGFAIPSNMVK 275
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                160 GIGFAIPSNMVK 171
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 SMART; SM00228; PL/Z;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          27
281
378
132
162
237
475 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Complete proteome.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   NCBI_TaxID=1360;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                HTRA_LACLA
Q9LA06;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         DOMAIN
ACT_SITE
ACT_SITE
ACT_SITE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       SIGNAL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           DOMAIN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             RESULT 4
HTRA_LACLA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        CHAIN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Matches
   [ 문 문 은 양 등
                                                                                          ò
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   g
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        A -> G (IN REF. 1).
STIYLLMQ -> RHLPVNAVISLNPFLKTGRGSPYNL (IN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             SEQUENCE FROM N.A.
STRAINFLT2 / SGS1412 / ATCC 700720;
MEDLINE-21534948; PubMed-11677609;
MEDLINE-21534948; PubMed-11677609;
MCDIELLand M., Sanderson K.E., Spieth J., Clifton S.W., Latreille P., Courtney L., Porwollik S., Ali J., Dante M., Du F., Hou S., Layman D., Leonard S., Mauyen C., Scott K., Holmes A., Grewal N., Milvaney E., Ryan E., Sun H., Florea L., Miller W., Stoneking T., Nhan M., Waterston R., Wilson R.K.;
Complete genome sequence of Salmonella enterica serovar Typhimurium
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Gaps
                                                                                                                                                                                                                                                                                                 Signal;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Johnson K., Charles I., Dougan G., Pickard D., O'Gaora P., Costa G., Ali T., Miller I., Hormaeche C.; "The role of a stress-response protein in Salmonella typhimurium
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Salmonella typhimurium.
<u>Bacteria</u>: Proteobacteria; gamma subdivision; Enterobacteriaceae;
Salmonella,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ;
0
                                                                                                                                                                                                                                                                                                                                                                                                         CHARGE RELAY SYSTEM (POTENTIAL).
CHARGE RELAY SYSTEM (POTENTIAL).
CHARGE RELAY SYSTEM (POTENTIAL).
                                                                                                                                                                                                                                     PRINTS; PR00834; PROTEASES2C.
SMART; SM00228; PDZ; 2.
PROSITE; PS50106; PDZ; 2.
Hydrolase; Serine protease; Heat shock; Periplasmic; Repeat;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Score 12; DB 1; Length 474;
Pred. No. 0.00024;
0; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                               A -> R (IN REF. 1, 7 AND 8).
E -> Q (IN REF. 7).
A -> G (IN REF. 1).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              5482E596F74B6D5F CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    01-AUG-1992 (Rel. 23, Created)
01-AUG-1992 (Rel. 23, Last sequence update)
15-JUN-2002 (Rel. 41, Last annotation update)
DEGP OR HTRA OR PTD OR STM0209.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       475 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Query Match 3.1%; Score 12; DB Best Local Similarity 100.0%; Pred. No. 0.0 Matches 12; Conservative 0; Mismatches
                                                                                                                                                                                                                                                                                                                                                     PROTEASE DO.
                                                                                                                                                                                 Interpro; IPR001254; Ser_protease_Try. Pfam; PF00089; trypsin; 1. PF00595; PDZ; 2.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                MEDLINE=91251770; PubMed=1645840;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Mol. Microbiol. 5:401-407(1991).
                                                                                                                                            InterPro; IPR001478; PDZ.
InterPro; IPR001940; Protease2C.
EMBL; AP002550; BAB33588.1; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              49354 MW;
               EMBL; M29955; AAA23717.1; -. EMBL; M31772; AAA23680.1; -.
                                                                                                      SWISS-2DPAGE; P09376; COLI.
EcoGene; EG10463; degP.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     STANDARD;
                                                                                                                                                                                                                                                                                                                                                                    371
371
131
131
161
236
10
46
474
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        160 GIGFAIPSNMVK 171
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             1111111111
263 GIGFAIPSNMVK 274
                                                    S01899; S01899.
B35993; B35993.
PS; S01.273; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              474 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                  Complete proteome.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            NCBI_Tax-TD=602;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               virulence."
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     DEGP_SALTY
P26982;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  STRAIN-C5;
                                                                                                                                                                                                                                                                                                                                                                                                           ACT_SITE
ACT_SITE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        CONFLICT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                ACT_SITE
                                                                                                                                                                                                                                                                                                                                                                                                                                                               CONFLICT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    CONFLICT
                                                                                          MEROPS;
                                                                                                                                                                                                                                                                                                                                                                      DOMAIN
                                                                                                                                                                                                                                                                                                                                     SIGNAL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                RESULT 3
DEGP_SALTY
```

g

ò

DOR WELL THE THE TELL THE TELL THE TELL THE TELL THE TELL THE THE TELL THE THE TELL THE THE TELL THE T

```
DEGP_BARHE
ID DEGP_BARHE
AC P54925;
                                                                                                                                                                                                                                                                                                                                                                                                                                                         ACT_SITE
ACT_SITE
SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                  ACT_SITE
                                                                                                                                                                                                                                                                                                                                                                                                               SIGNAL
                                                                                                                                                                                                                                                                                                                                                                                                                                DOMAIN
                                                                                                                                                                                                                                                                                                                                                                                                                                         DOMAIN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           RESULT 6
 QQ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ó
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             BETTT
                                                                                                                                       This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation—the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to licenseeisb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                ö
                        Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Bacteria; Proteobacteria; gamma subdivision; Enterobacteriaceae;
Escherichia.
                                                                                                                                                                                                                                                                                                                                                                                                               ö
                                                                                                                                                                                                                                                                                                                                               CHARGE RELAY SYSTEM (POTENTIAL).
CHARGE RELAY SYSTEM (POTENTIAL).
CHARGE RELAY SYSTEM (POTENTIAL).
581B90B55A7DF851 CRC64;
                                                                                                                                                                                                                                                                                                              Hydrolase; Serine protease; Transmembrane; Complete proteome.
TRANSMEM 6 26 26
                                                                                                                                                                                                                                                                                                                                                                                            Length 408;
                                                                                                                                                                                                                                                                                                                                                                                    Score 11; DB 1; Lengtn 400; Pred. No. 0.0023;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Bass S., Gu O., Goddard A.;
Submitted (OCT-1994) to the EMBL/GenBank/DDBJ databases
                                                                                                      -!- SUBCELLUIAR LOCATION: Membrane-bound (Probable).
-!- SIMILARITY: BELONGS TO PEPTIDASE FAMILY S2C.
-!- SIMILARITY: CONTAINS 1 PDZ/DHR DOMAIN.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         01-FEB-1995 (Rel. 31, Created)
01-FEB-1995 (Rel. 31, Last sequence update)
15-JUN-2002 (Rel. 41, Last annotation update)
DEGQ OR HHOA OR B3234.
                                                                                                                                                                                                                                                                                                                                                                                      2.8%; Sco. 100.0%; Pred. No. ...
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             SEQUENCE FROM N.A., AND SEQUENCE OF 28-32.
                                                                                                                                                                                                                                                                                                                                CATALYTIC
                                                                                                                                                                                                                                   InterPro; IPR001478; PDZ.
InterPro; IPR001940; Protease2C.
InterPro; IPR001254; Ser_protease_Try.
Pfam; PF00089; trypsin; 1.
                MEDLINE-21235186; PubMed-11337471;
                                                                                                                                                                                                             EMBL; AF155705; AAF61294.1; -. EMBL; AE006442; AAK06234.1; -.
                                                                                                                                                                                                                                                                                                                                                                           41648 MW;
                                                                                                                                                                                                                                                                                    PRINTS; PR00834; PROTEASES2C.
SMART; SM00228; PDZ; 1.
PROSITE; PS50106; PDZ; 1.
                                                                                                                                                                                                                                                                                                                                                                                                              11; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            STANDARD;
                                                                                                                                                                                                                                                                                                                                                                                                    Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                              128 INPGNSGGALI 138
                                                                                                                                                                                                                                                                                                                                                                                                                                        111111111
234 INPGNSGGALI 244
                                                                                                                                                                                                                                                                                                                                        302
127
157
239
408 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           STRAIN-K12 / W3110;
SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   SEQUENCE FROM N.A.
                                                                                                                                                                                                                                 MEROPS; S01,273;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Escherichia coli
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   NCBI_TaxID=562;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         DEGO_ECOLI
P39099;
                                                                                                                                                                                                                                                                                                                                                        ACT_SITE
ACT_SITE
SEQUENCE
                                                                                                                                                                                                                                                                                                                                                   ACT_SITE
                                                                                                                                                                                                                                                                                                                                                                                            Query Match
                                                                                                                                                                                                                                                                                                                                DOMAIN
                                                                                                                                                                                                                                                                                                                                        DOMAIN
                                                                                                                                                                                                                                                                                                                                                                                                              Matches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                           RESULT
                                                                                                                                                                                                                                                                                                                                                                                                      Best
ò
                                                                                                                                                                                                                                                                                                                                                                                                                                               음
```

```
This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation - the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ö
                                                                                                                                                                                                          SEQUENCE FROM N.A.

SEQUENCE FROM N.A.

SEQUENCE TO MG1655;

MEDLINE-97426611; PubMed=9278503;

MEDLINE-97426611; PubMed=9278503;

Blattner F.R., Plunkett G. III, Bloch C.A., Perna N.T., Burland V.,

Riley M., Collado-Vides J., Glasner J.D., Rode C.K., Mayhew G.F.,

A Gregor J., Davis N.W., Kirkpatrick H.A., Goeden M.A., Rose D.J.,

Mau B., Shao Y.;

The complete genome sequence of Escherichia coli K-12.";

Science 277:1453-1474(1997).

C -i- FUNCTION: PROTEASE WITH A SHARED SPECIFICITY WITH DEGP/DEGP.

-i- SUBCELLULAR LOCATION: Periplasmic.

C -i- SIMILARITY: BELONGS TO PERIDASE FAMILY S2C.

C -i- SIMILARITY: CONTAINS 2 PDZ/DHR DOMAINS.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   01-0CT-1996 (Rel. 34, Created)
01-0CT-1996 (Rel. 34, Last sequence update)
15-JUN-2002 (Rel. 41, Last annotation update)
Probable periplasmic serine protease DO-like precursor (EC 3.4.21.-)
(Antigen htrA).
STRAIN-K12 / W3110;
MEDLINE-96165272; PubMed-8576051;
Waller P.R., Sauer R.T.;
"Characterization of degQ and degS, Escherichia coli genes encoding homologs of the DegP protease.";
J. Bacteriol. 178:1146-1153(1996).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                CHARGE RELAY SYSTEM (POTENTIAL).
CHARGE RELAY SYSTEM (POTENTIAL).
CHARGE RELAY SYSTEM (POTENTIAL).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Score 11; DB 1; Length 455; Pred. No. 0.0026; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Hydrolase; Serine protease; Periplasmic; Repeat; Signal; Complete proteome.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               6A090F93AC021C83 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     2.8%; Scor.
100.0%; Pred. No. v...
0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              503 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           PROTEASE DEGO
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                EcoGene, EG12612; deg0.
InterPro; IPR001478; PD2.
InterPro; IPR001940; Protesse2C.
InterPro; IPR001254; Ser_protesse_Try.
Pfam; PF00089; trypsin; 1.
Pfam; PF00595; PD2; 2.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               47205 MW;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     EMBL; U15661; AAC43992.1; -. EMBL; U32495; AAC44005.1; -. EMBL; U18997; AAA58036.1; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          PRINTS; PR00834; PROTEASES2C. SMART; SM00228; PDZ; 2.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    EMBL; AE000402; AAC76266.1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                MEROPS; S01.274; -. SWISS-2DPAGE; P39099; COLI.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Query Match 2.8
Best Local Similarity 100.
Matches 11; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 STANDARD;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      PROSITE; PS50106; PDZ;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                119 ENFIQTDASIN 129
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                139
214
25 AA;
```

S

```
92
122
197
340 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          120 NFIQTDASIN 129
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              184 NFIQTDASIN 193
                                                                                                                                                                                                                                                              MEROPS; S01.275; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         [1]
SEQUENCE FROM N.A.
STRAIN-168;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Bacillus subtilis.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       [2]
SEQUENCE FROM N.A.
                                                                                   Venter J.C.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               YYXA OR YYCK
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 YYXA_BACSU
P39668;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      10;
                                                                                                                                                                                                                                                                                                                                                                                                             ACT_SITE
ACT_SITE
                                                                                                                                                                                                                                                                                                                                                                                                                                  ACT_SITE
SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Local
                                                                                                                                                                                                                                                                                                                                                                                SIGNAL
                                                                                                                                                                                                                                                                                                                                                                                                     DOMAIN
                                                                                                                                                                                                                                                                                                                                                                                          CHAIN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        YYXA_BACSU
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Matches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             RESULT 8
 ŏ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            g
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the BMBL outstation. the Buropean Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no-way modified and this statement is not removed. Usage by and for-commercial entities requires a license agreement (see http://www.isb.sib.ch/announce/or send an email to licenseelab-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ó
                                                                   STRAIN-Houston-1;
MEDLINE-94299828; PubMed-8027347;
Anderson B., Sims K., Regnery R., Robinson L., Schmidt M.J.,
Anderson B., Hager C., Edwards K.;
"Detection of Rochallmaea henselae DNA in specimens from cat scratch
disease patients by PCR.";
J. Clin. Microbiol. 32:942-948(194).
I- SUBCELLULAR LOCATION: Periphasmic (Potential).
I- SIMILARITY: BELONGS TO PEPPILDASE FAMILY S2C.
I- SIMILARITY: CONTAINS 2 PDZ/DHR DOMAINS.
                                                                                                                                                                                                                                                                                                                                                                                                  PROBABLE PERIPLASMIC SERINE PROTEASE DO-
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Gaps
        Bartonella henselae (Rochalimaea henselae).
Bacteria; Proteobacteria; alpha subdivision; Rhizobiaceae group;
Bartonellaceae; Bartonella.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ;
0
                                                                                                                                                                                                                                                                                                                                                                                                                                         CHARGE RELAY SYSTEM (POTENTIAL).
CHARGE RELAY SYSTEM (POTENTIAL).
GCD9F4743282AF9E CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Bacteria; Proteobacteria; gamma subdivision; Pasteurellaceae;
Haemophilus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      DB 1; Lens.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Length 503;
                                                                                                                                                                                                                                                                                                                                                                              Periplasmic; Repeat; Signal.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            01-NOV-1995 (Rel. 32, Last sequence update)
15-JUN-2002 (Rel. 41, Last annotation update)
Protease degS precursor (EC 3.4.21.-).
DEGS OR HHOB OR HTRH OR HI0945.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Score 11; DB 1; Pred. No. 0.0000; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               340 AA
                                                                                                                                                                                                                                                                                         InterPro; IPR001478; PDZ.
InterPro; IPR001340; Protease2C.
InterPro; IPR001340; Protease_Try.
Pfam; PF00089; trypsin; 1.
Pfam; PF00089; trypsin; 1.
Pfam; PF00084; PZ, 2.
PRINTS; PR00834; PROFESESZC.
SMART; SM00228; PDZ, 2.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    STRAIN-Rd / KW20 / ATCC 51907;
MEDLINE=95350630; PubMed=7542800;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   01-NOV-1995 (Rel. 32, Created)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                          54114 MW;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             2.8%; ;
100.0%;
                                                                                                                                                                                                                                                                     EMBL; L20127; AAA97430.1; -.
                                                                                                                                                                                                                                                                                                                                                                              Hydrolase; Serine protease;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Local Similarity 100.
Les 11; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               STANDARD;
                                                                                                                                                                                                                                                                                                                                                                  PROSITE; PS50106; PDZ;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Haemophilus influenzae
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  135 DGYIVTNNHVI 145
                                                                                                                                                                                                                                                                                                                                                                                                                                                   173
247
503 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       20 DGYIVTNNHVI 30
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          SEQUENCE FROM N.A.
                                                          SEQUENCE FROM N.A.
                                      NCBI_TaxID=38323;
                                                                                                                                                                                                                                                                                                                                                                                                 19
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       NCBI_TaxID=727;
                                                                                                                                                                                                                                                                                  MEROPS; S01,273
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              DEGS_HAEIN
P44947;
                                                                                                                                                                                                                                                                                                                                                                                                                                           ACT_SITE
ACT_SITE
ACT_SITE
SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Best Local
Matches
                                                                                                                                                                                                                                                                                                                                                                                        SIGNAL
                                                                                                                                                                                                                                                                                                                                                                                                                       DOMAIN
                                                                                                                                                                                                                                                                                                                                                                                                                                  DOMAIN
                                                                                                                                                                                                                                                                                                                                                                                                  CHAIN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   DEGS_HAEIN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          RESULT 7
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          g
ò
```

This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation-the-European Bioinformatics. Institute. There are no restrictions on its use by non-profit institutions, as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/ ö 'Whole-genome random sequencing and assembly of Haemophilus influenzae Fleischmann R.D., Adams M.D., White O., Clayton R.A., Kirkness E.F., Kerlavage A.R., Bult C.J., Tomb J.-F., Dougherty B.A., Merrick J.M., McKenney K., Sutton G., Fitzhugh W., Fields C.A., Gocayne J.D., Scott J.D., Sharley R., Liu L.-I., Glodek A., Kelley J.M., Weidman J.F., Phillips C.A., Spriggs T., Hedblom E., Cotton M.D., Utterback T.K., Hanna M.C., Nguyen D.T., Sauddek D.M., Brandon R.C., Fine L.D., Fritchman J.L., Fuhrmann J.L., Geoghagen N.S.M., Gnehm C.L., McDonald L.A., Small K.V., Fraser C.M., Smith H.O., Gaps PROSITE; PS50106; PD2; 1. Hydrolase; Serine protease; Periplasmic; Signal; Complete proteome. ó STRAIN-10b;
Kasahara Y., Nakai S., Yoshikawa H., Ogasawara N.;
"36kb sequence between gntZ and trnY of B. subtilis genome.";
Submitted (NOV-1995) to the EMBL/GenBank/DDBJ databases. CHARGE RELAY SYSTEM (POTENTIAL)
CHARGE RELAY SYSTEM (POTENTIAL)
69EA452DF5A10649 CRC64; CHARGE RELAY SYSTEM (POTENTIAL) Length 340; Score 10; DB 1; Leng...
Tred. No. 0.022;
0; Indels Bacteria; Firmicutes; Bacillales; Bacillaceae; Bacillus. NCBI_TaxID=1423; Science 269:496-512(1995).

- SUBCELLOLAR LOCATION: Periplasmic (Potential).
- SUBLERITY: BELONGS TO PEPTIDASE FAMILY S2C.
- SIMILARITY: CONTAINS 1 PDZ/DHR DOMAIN. 01-FEB-1995 (Rel. 31, Created)
01-6CT-1996 (Rel. 34, Last sequence update)
15-UTN-2002 (Rel. 41, Last annotation update)
Hypothetical serine protease yyxk (EC 3.4.21.-). 400 AA PROTEASE DEGS. or send an email to license@isb-sib.ch). TIGR; H10945; -.
InterPro; IPR001478; PDZ.
InterPro; IPR001940; Protease2C.
InterPro; IPR001254; Ser_protease_Try.
Pfam; PF00089; trypisin; 1.
Pfam; PF00595; PDZ, 1. POTENTIAL 2.6%; Scc. 100.0%; Pre 0;) 36039 MW; PRINTS; PR00834; PROTEASES2C. SMART; SM00228; PD:: 1. PROSITE; PS50106; PDZ; 1. EMBL; U32775; AAC2::599.1; -. Conservative STANDARD;

243 CHARGE RELAY SYSTEM (POTENTIAL). 42788 MW; 91A6E0E897B6F64C CRC64;

ACT_SITE SEQUENCE

```
RESULT 10
DEGP_CHLPN
                                A Kunst F., Ogasawara N., Moszar I., Alberthni A.M., Alloni G.,
Azevedo V., Bertero M.G., Bessieres P., Bolotin A., Borchert S.,
Ra Azevedo V., Bertero M.G., Bessieres P., Bolotin A., Borchert S.,
Ra Borriss R., Bourster L., Brans A., Braun M., Brignell S.C., Bron S.,
Ra Brouillet S., Bruschi C.V., Caldwell B., Capuano V., Carter N.M.,
RA Brouillet S., Bringhow J., Connerton I.F., Cummings N.J., Daniel R.A.,
RA Broizof F. V., Deviner K.M., Dusterhoft A., Ehrlich S.D., Emmerson P.T.,
RA Britz C., Fujita M., Fujita Y., Fuma S., Galizzi A., Galleron N.,
RA Fritz C., Fujita M., Fujita Y., Fuma S., Galizzi A., Galleron N.,
RA Guiseppi G., Guy B.J., Haga K., Haiech J., Harwood C.R., Henaut A.,
A Hilbert H., Holsapel S., Hosono S., Hullo M.F., Itaya M., Jones L.,
RA Guiseppi G., Guy B.J., Haga K., Haiech J., Harwood C.R., Henaut A.,
A Kramate D., Kasahara Y., Klaerr-Blanchard M., Klein C.,
RA Kobayashi Y., Koetter P., Koningstein G., Krogh S., Kumano M.,
Rurita K., Levine A., Liu H., Masuda S., Mauel C., Medigue C.,
A Kurita K., Levine A., Liu H., Masuda S., Mauel C., Medigue C.,
RA Moone D., O'Reilly M., Ogawa K., Ogiwara A., Oudega B., Park S.H.,
RA Reger M., Rivolta C., Rocha E., Roche B., Rose M., Sadaie Y.,
Santo T., Scanlan E., Schleich S., Schroeter R., Scoffone F.,
Sato T., Scanlan E., Schleich S., Schroeter R., Scoffone F.,
Sato T., Scanlan S., Vandenbol M., Vandamut K.,
A Tarakoto W., Uchiyama S., Vandenbol M., Vandama H., Tarkman H., Parkman Positive bacterium Bacillus R., Wallin R., Washikawa H., Danchin A.,
RY Subhila S., Waller E., Wedler E., Wedle
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation—the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      "Rock, a novel regulatory protein controlling arginine utilization in Bacillus subtilis, belongs to the NtrC/NifA family of transcriptional
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               PROSITE; PS50106; PD2; FALSE_NEG.
Hypothetical protein; Hydrolase; Serine protease; Transmembrane;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Calogero S., Gardan R., Glaser P., Schweitzer J., Rapoport G., Debarbouille M.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      POTENTIAL,
CHARGE RELAY SYSTEM (POTENTIAL).
CHARGE RELAY SYSTEM (POTENTIAL).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    activators.";
J. Bacteriol. 176:1234-1241(1994).
-!- SUBCELLULAR LOCATION: Membrane-bound (Potential).
-!- SIMILARITY: BELONGS TO PEPTIDASE FAMILY S2C.
-!- SIMILARITY: CONTAINS 1 PDZ/DHR DOMAIN.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Subtilist; BG11054; yyxA.
InterPro; IPR001478; PDZ.
InterPro; IPR001940; Protesse2C.
InterPro; IPR001254; Ser_protesse_Try.
Pfam; PF00089; trypsin; 1.
Pfam; PF00595; PDZ; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          EMBL; 299124; CAB16073.1; -. EMBL; L22006; -; NOT_ANNOTATED_CDS.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           STRAIN-168 / Marburg;
MEDLINE-94156824; PubMed-8113162;
                    MEDLINE-98044033; PubMed-9384377;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 SEQUENCE OF 317-400 FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 PRINTS; PR00834; PROTEASES2C.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     EMBL; D78193; BAA11295.1; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Nature 390:249-256(1997).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             SMART; SM00228; PDZ;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Complete proteome
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          MEROPS; S01.273;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ACT_SITE
ACT_SITE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         TRANSMEM
```

```
This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation - the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
                                          ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ö
                                            Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Gaps
                                            ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         CHARGE RELAY SYSTEM (POTENTIAL).
CHARGE RELAY SYSTEM (POTENTIAL).
CHARGE RELAY SYSTEM (POTENTIAL).
B168677991C88707 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                             Smeds A., Varmanen P.K., Palva A.M.;
"Molecular characterization of a stress-inducible gene from
"Lactobacillus helveticus.",
J. Bacteriol. 180:6143-6153(1998).
--- SUBCELLULAR LOCATION: Membrane-bound (Potential).
--- SIMILARITY: BELONGS TO PEPTIDASE FAMILY $2C.
--- SIMILARITY: CONTAINS I PDZ/DHR DOMAIN.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     2.6%; Score 10; DB 1; Length 413; 00.0%; Pred. No. 0.026;
            Length 400;
                                            Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   0; Indels
                                                                                                                                                                                                                                                                                                   Bacteria; Firmicutes; Lactobacillales; Lactobacillaceae;
Lactobacillus.
DB 1; Leus.
                                                                                                                                                                                                             16-OCT-2001 (Rel. 40, Created)
16-OCT-2001 (Rel. 40, Last sequence update)
16-OCT-2002 (Rel. 41, Last annotation update)
Serine protease do-like htrA (EC 3.4.21.).
           2.6%; Score 10; DB 100.0%; Pred. No. 0.0 tive 0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     100.0%; Pred. No. 0.0 ive 0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Hydrolase, Serine protease, Transmembrane.
TRANSMEM 20 40 POTENTIAL.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              CATALYTIC.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       MEROPS; SO1.273; -.
InterPro; IRROD1478; PDZ.
InterPro; IPRO01474; Ser_protease_Try.
Pfam; PF00089; trypsin; 1.
Pfam; PF00228; PDZ; 1.
SMART: SMO0228; PDZ; 1.
PROSITE; PS50106; PDZ; 1.
                                                                                                                                                                                                                                                                                                                                                                                                MEDLINE-99047559; PubMed-9829922;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         EMBL; AJ005672; CAA06668.1; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         42647 MW;
                            Best Local Similarity 100.0
Matches 10; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Best Local Similarity 100.0
Matches 10; Conservative
                                                                                                                                                                                   STANDARD;
                                                                                                                                                                                                                                                                                        Lactobacillus helveticus
                                                                       128 INPGNSGGAL 137
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         150
180
258
413 AA;
                                                                                                     238 INPGNSGGAL 247
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 143 GYIVTNNHVI 152
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 21 GYIVTNNHVI 30
                                                                                                                                                                                                                                                                                                                                                                    SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                      NCBI_TaxID=1587;
                                                                                                                                                                                 HTRA_LACHE
Q924H7;
                                                                                                                                                                                                                                                                                                                                                                                    STRAIN=53/7
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ACT_SITE
ACT_SITE
ACT_SITE
SEQUENCE
              Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 DOMAIN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              DOMAIN
                                                                                                                                                    RESULT 9
HTRA_LACHE
                                                                          ò
                                                                                                                                                                                   ò
```

488 AA; 52311 MW; OEE7E0F88F106F49 CRC64;

```
SEQUENCE
                   Query Match
                                         Matches
                                                                                                                 RESULT 11
 S
                                                                                                                                               g
                                                                                                                                                                                                                                                                                                                                                                                                                                          This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation-the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                            Read T.D., Brunham R.C., Shen C., Gill S.R., Heidelberg J.F.,
White O., Hickey E.K., Peterson J., Utterback T., Berry K., Bass S.,
Linher K., Weidman J., Khouri H., Craven B., Bowman C., Dodson R.,
Gwinn M., Nelson W., DeBoy R., Kolonay J., McClarty G., Salzberg S.L.,
Eisen J., Fraser C.M.;
"Genome sequences of Chlamydia trachomatis MoPn and Chlamydia
pneumoniae AR39.";
                                                                                                                                                                                                                                                                                                                                    Kalman S., Mitchell W., Marathe R., Lammel C., Fan J., Hyman R.W., Olinger L., Grimwood J., Davis R.W., Stephens R.S.; "Comparative genomes of Chlamydia pneumoniae and C. trachomatis."; Nat. Genet. 21:385-389(1999).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Repeat; Signal; Complete proteome.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        POTENTIAL.
PROBABLE SERINE PROTEASE DO-LIKE.
CATALYTIC.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          RELAY SYSTEM (POTENTIAL).
RELAY SYSTEM (POTENTIAL).
RELAY SYSTEM (POTENTIAL).
                                               Probable serine protease do-11ke precursor (EC 3.4.21.-).
DEGP OR HTRA OR CPN0979 OR CP0877.
                                                                     Chlamydia pneumoniae (Chlamydophila pneumoniae).
Bacteria; Chlamydiales; Chlamydiaceae; Chlamydophila.
NCBI_TaxID=83558;
       0926T0; 09JQD7; 09KIW4;
16-0CT-2001 (Rel. 40, Created)
16-CCT-2001 (Rel. 40, Last sequence update)
15-JUN-2002 (Rel. 41, Last annotation update)
488 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        InterPro; IPR001478; PDZ.
InterPro; IPR001940; Protease2C.
InterPro; IPR001254; Ser_protease_Try.
                                                                                                                                                                                                                                                                                                        Nucleic Acids Res. 28:1397-1406(2000).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          CHARGE F
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      PDZ 1.
PDZ 2.
                                                                                                                         STRAIN-CWL029;
MEDLINE-99206606; Pubmed-10192388;
                                                                                                                                                                                                                      MEDLINE-20150255; PubMed-10684935;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            EMBL; AE001678; AAD19116.1; -. EMBL; AE002246; AAF38665.1; -. EMBL; AP002548; BAA99186.1; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           PRINTS; PRO0834; PROTEASES2C.
SMART; SM00228; PDZ; 2.
PROSITE; PS50106; PDZ; 2.
Hydrolase; Serine protease; R
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Pfam; PF00089; trypsin; 1.
Pfam; PF00595; PDZ; 2.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           MEROPS; S01.273; -.
PHCI-2DPAGE; Q9Z6T0; -.
TIGR; CP0877; -.
                                                                                                               SEQUENCE FROM N.A.
                                                                                                                                                                                                SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                          SEQUENCE FROM N.A.
                                                                                                                                                                                                            STRAIN-AR39
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            DOMAIN
DOMAIN
DOMAIN
ACT_SITE
ACT_SITE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         SIGNAL
```

```
ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the Buropean Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@ib-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           CAN DEGRADE BEYA-CASEIN.
-!- ENLYME REGULATION: INHIBITED BY PHENYLMETHYLSULFONYL FLUORIDE AND
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Arabidopsis thaliana (Mouse-ear cress).
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; Rosidae;
eurosids II; Brassicales; Brassicaceae; Arabidopsis.
                                                                                                                                  Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         STRAIN-cv. Columbia;
Kieselbach T., Bystedt M., Schroeder W.P.;
Submitted (JUL-2001) to the SWISS-PROF data bank.
-!- FUNCTION: SERIHE PROFESSE THAT IS REQUIRED AT HIGH TEMPERATURE.
MAY BE INVOLVED IN THE DEGRADATION OF DAMAGED PROTEINS. IN VIVO,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     STRAIN-CV. Columbia;
MEDLINE-20363099; FubMed=10907853;
Raneko T., Katoh T., Sato S., Nakamura A., Asamizu E., Tabata S.;
"Structural analysis of Arabidopsis thaliana chromosome 3. II.
Sequence features of Arabidopsis by regions covered by 90 Pl, TAC and BAC clones.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           -!- SUBCELLULAR LOCATION: BOUND TO LUMINAL SIDE OF THE THYLAKOID
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   SEQUENCE FROM N.A., AND CHARACTERIZATION.
MEDLINE-98175982; FubMed-9507020;
Itzhaki H., Naveh I., Lindahl M., Cook M., Adam Z.;
"Identification and characterization of DegP, a serine protease associated with the luminal side of the thylakoid membrane.";
J. Biol. Chem. 273:7094-7098(1998).
                                                                                                                           ö
      Length 488;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        DEG1_ARATH STANDARD; PRT; 437 AA.
022609. 09LK85;
16-0CT-2001 (Rel. 40, Created)
16-0CT-2001 (Rel. 40, Last sequence update)
15-JUN-2002 (Rel. 41, Last annotation update)
Protease Do-like 1, chloroplast precursor (EC 3.4.21.-).
DEGPI OR DEGP OR AJ3G27925 OR K16N12.18.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             -!- INDUCTION: BY HEAT SHOCK.
-!- SIMILARITY: BELONGS TO PEPTIDASE FAMILY S2C.
-!- SIMILARITY: CONTAINS 1 PDZ/DHR DOMAIN.
2.6%; Score 10; DB 1;
100.0%; Pred. No. 0.031;
tive 0; Mismatches C
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     InterPro; IPR001478; PDZ.
InterPro; IPR001940; Protease2C.
InterPro; IPR001254; Ser_protease_Try.
Pfam: PF000089; trypsin; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              EMBL; AF028842; AA:39436.1; -- BMBL; AP000371; BA302539.1; -- BMBL; AP001302; BA302539.1; JOINED. MEROPS; S01.279; -- AP001379; -- AP00
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               DNA Res. 7:217-221(2000).
                                                                                                                           Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          [3]
SEQUENCE OF 104-118.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             O-PHENANTHROLINE
                                                                                                                                                                                                                                                                                                                        126 DGYIVTNNHV 135
                                                          Local Similarity
                                                                                                                                                                                                                                                       20 DGYIVTNNHV 29
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              NCBI_TaxID=3702;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         MEMBRANE.
                                                                                                                     10;
```

```
STRAIN-168;
                                                                                                                                                                                                                                                                                                               STRAIN-168
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           STRAIN-168
     ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Kunst F., Ogasawara N., Moser I., Alberthni A.M., Alloni G.,
Azevedo V., Bertero M.G., Bessieres P., Bolotin A., Borchert S.,
A Zevedo V., Bertero M.G., Caldwell B., Bolotin A., Borchert S.,
Borriss R., Boursier L., Caldwell B., Capuano V., Carter N.M.,
A Groi S.K., Codani J.J., Connerton I.F., Cummings N.J., Daniel R.A.,
Choi S.K., Cadani J.J., Connerton I.F., Cummings N.J., Daniel R.A.,
Choi S.K., Cadani J.J., Connerton I.F., Cummings N.J., Ennerson P.T.,
A Entian K.D., Errington J., Fabret C., Ferrari E., Foulger D.,
A Fritz C., Fujita M., Fujita Y., Fuma S., Galizzi A., Galleron N.,
A Guiseppi G., Guy B.J., Haga K., Halech J., Harwood C.R., Henaut A.,
Joris B., Karamata D., Kasahara Y., Klaerr-Blanchard M., Klein C.,
A Kobayashi Y., Koetter P., Koningstein G., Kroph S., Kumano M.,
Kurita K., Layldus A., Lardinois S., Lauber J., Lazarevic V.,
A Kurita K., Levine A., Lulu H., Masuda S., Mauel C., Medique C.,
A Medina N., Mellado R.P., Mizuno M., Moestl D., Nakai S., Noback M.,
Noone D., O'Reilly M., Ogawa K., Ogiwara A., Oudega B., Park S.H.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Gaps
                                                                           Transit peptide; Chloroplast; Thylakoid.
CHLOROPLAST (POTENTIAL).
                                                                                                                                                                                          CHARGE RELAY SYSTEM (POTENTIAL).
CHARGE RELAY SYSTEM (POTENTIAL).
CHARGE RELAY SYSTEM (POTENTIAL).
HSPPSSQLSNST -> SSTLEHLRSPESHL (IN REF.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              "Sequence of the Bacillus subtilis genome between xlyA and ykoR."; Submitted (NOV-1997) to the EMBL/GenBank/DDBJ databases.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  DB 1; Length 437; 0.31;
                                                                                                                                                                                                                                                                     2).

V -> I (IN REF. 2).

P -> S (IN REF. 2).

G -> R (IN REF. 2).

LL -> HF (IN REF. 2).

LL -> V (IN REF. 2).

I -> V (IN REF. 2).

I -> V (IN REF. 2).

G -> E (IN REF. 2).

M, 1497Blab3F5FF2A4 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Firmicutes; Bacillales; Bacillaceae; Bacillus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                15-JUN-2002 (Rel. 41, Created)
15-JUN-2002 (Rel. 41, Last sequence update)
15-JUN-2002 (Rel. 41, Last annotation update)
Probable serine protease do-like htrA (EC 3.4.21.-).
                                                                                                                                    PROTEASE DO-LIKE 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                        2.3%; Score ,,
100.0%; Pred. No. 0.31;
--**... 0; Mismatches
                                                                                                                                                          SERINE PROTEASE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                449 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          STRAIN-168;
MEDLINE-98044033; PubMed-9384377;
                                                                                                                                                                                                                                                                                                                                                                                                                                              46213 MW;
Pfam; PF00595; PDZ; 1.
PRINTS; PR00B34; PR0TEASES2C.
SMART; SM00228; PDZ; 1.
PROSITE; PS50106; PDZ; 1.
                                                                             Hydrolase; Serine protease;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      9; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                STANDARD;
                                                                                                                                                                                                                                                                                         36
54
60
69
                                                                                                                                                                                                                                                                                                                                                                                                                                        437 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 11111111
231 VFAIGNPFG 239
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Bacillus subtilis.
Bacteria; Firmicut
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           87 VFAIGNPFG 95
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     NCBI_TaxID-1423;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Devine K.M.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            HTRA_BACSU
034358;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            STRAIN=168;
                                                                                                                                                                                                            ACT_SITE
ACT_SITE
CONFLICT
                                                                                                                                                                                                                                                                                                                             CONFLICT
CONFLICT
CONFLICT
CONFLICT
CONFLICT
CONFLICT
SEQUENCE
                                                                                                                                                                                              ACT_SITE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Query Match
                                                                                                                                                                                                                                                                                         CONFLICT
                                                                                                                                                                                                                                                                                                             CONFLICT
                                                                                                                   FRANSIT
                                                                                                 FRANSIT
                                                                                                                                                      DOMAIN
                                                                                                                                      CHAIN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Matches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        RESULT 12
 ò
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               g
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ACCOORDING TO THE LANGE OF THE
```

```
This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             -:- SUBCELLULAR LOCATION: Membrane-bound (Potential).
-:- INDUCTION: Transcription is cssS dependent. Induced by heat shock during exponential growth and by heterologous amylases at the transition phase of the growth cycle. Negatively regulates its own expression during exponential growth and during heat shock.
-:- MISCELLANDOUS: Inactivation results in compensating overexpression of ytvA, especially during stress conditions.
-:- SIMILARITY: BELONGS TO PEPTIDASE FAMILY S2C.
Parro V., Pohl T.M., Portetelle D., Porwollik S., Prescott A.M., Presecan E., Pujic P., Purnelle B., Rapoport G., Rey M., Reynolds S., Rieger M., Rivolta C., Rocha E., Roche B., Rose M., Sadale Y., Sato T., Scanlan E., Schleich S., Schroeter R., Scoffone F., Sekiguchi J., Sekowska A., Seror S.J., Serror P., Shin B.S., Soldo B., Sorokin A., Tacconi E., Takagia T., Takahashi H., Takemaru K., Takeuchi M., Tanaka T., Terpstra P., Tognoni A., Tosato V., Uchiyama S., Vandenbol M., Vannier P., Vassarotti A., Vianut R., Wedler E., Wedler H., Weitzenegger T., Winters P., Wipat A., Yamamoto H., Yamane K., Yasumoto K., Yata K., Yoshida K., Yoshikawa H.F., Zumsteln E., Yoshikawa H., Danchin A.; The complete genome sequence of the Gram-positive bacterium Bacillus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   "A novel two-component regulatory system in Bacillus subtilis for the survival of severe secretion stress.";
Mol. Microbiol. 41:1159-1172(2001).
-!- FUNCTION: May be involved in processing, maturation, or secretion of extracellular enzymes.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Noone D., Howell A., Collery R., Devine K.M.;
"YkdA and YvtA, HtrA-like serine proteases in Bacillus subtills, engage in negative autoregulation and reciprocal cross-regulation of ykdA and yvtA gene expression.";
"J. Bacteriol. 183:654-663(2001)."
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Noone D., Howell A., Devine K.M.; "Expression of ykdA, encoding a Bacillus subtilis homologue of HtrA, is heat shock inducible and negatively autoregulated."; J. Bacteriol. 182:1592-1599(2000).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Hyyrylaeinen H.-L., Bolhuis A., Darmon E., Muukkonen L., Koski P., Vitikainen M., Sarvas M., Pragai Z., Bron S., van Diji J.M., Kontinen V.P.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              MEROPS; SO1.273; -. Subtlinst; BG122608; htra.
Subtlinist; BG122608; htra.
InterPro; IPR001478; PDZ.
InterPro; IPR001940; Protease2C.
InterPro; IPR001254; Ser_protease_Try.
Pfam; PF00089; trypsin; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            EMBL; AJ002571; CAA05570.1; -. EMBL; 299110; CAB13147.1; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    PRINTS; PR00834; PROTEASES2C.
SMART; SM00228; PDZ; 1.
PROSITE; PS50106; PDZ; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      TRANSCRIPTIONAL REGULATION.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              TRANSCRIPTIONAL REGULATION.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      TRANSCRIPTIONAL REGULATION
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       subtilis.";
Nature 390:249-256(1997).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       PubMed-11133960;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        PubMed=10692364;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         PubMed-11555295;
```

σ

ö

Gaps

Length 478;

DB 1; . 0.34;

```
478 AA; 52230 MW; 868E8732CAC50629 CRC64;
                                     Conservative
                   Query Match
Best Local Similarity
Matches 9; Conserv
                                                       9 RALGSGVII 17
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          CHAIN
DOMAIN
DOMAIN
DOMAIN
ACT_SITE
ACT_SITE
ACT_SITE
SCUENCE
 SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  SIGNAL
                                                                                                              DEGP_BUCAP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               RESULT 15
                                                                                                      RESULT 14
 So
                                                                        g
                                                                                                                        ŏ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   qq
                                                         ŏ
                                                                                                                                                                                                                                                                                                                                                                                                                               This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (see http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
                                                                                                                                         ô
                                                                                                                                                                                                                                                                                         Buchnera aphidicola (subsp. Acyrthosiphon pisum) (Acyrthosiphon pisum
                                                                                                                                         Gaps
                                                                                                                                                                                                                                                                                                                                   Hydrolase; Protease; Serine protease; Heat shock; Transmembrane;
                                                                                                                                         ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Repeat; Signal; Complete proteome.
POTENTIAL.
PROBABLE SERINE PROTEASE DO-LIKE.
                                                                       CHARGE RELAY SYSTEM (POTENTIAL).
CHARGE RELAY SYSTEM (POTENTIAL).
CHARGE RELAY SYSTEM (POTENTIAL).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           CHARGE RELAY SYSTEM (POTENTIAL).
CHARGE RELAY SYSTEM (POTENTIAL).
CHARGE RELAY SYSTEM (POTENTIAL).
                                                                                                                                                                                                                                           16-OCT-2001 (Rel. 40, Created)
16-OCT-2001 (Rel. 40, Last sequence update)
15-JUN-2002 (Rel. 41, Last annotation update)
Probable serine protease do-like precursor (EC 3.4.21.-).
                                                                                                                     2.3%; Score 9; DB 1; Length 449; 00.0%; Pred. No. 0.32;
                                                                                                                                         0; Indels
                                                                                                    E12B07A9018EE414 CRC64;
                           POTENTIAL.
EXTRACELLULAR (POTENTIAL)
                                                                                                                                                                                                                                                                                                  symbiotic bacterium).
Bacteria; Proteobacteria; gamma subdivision; Buchnera.
NCBI_TaxID=118099;
                   CYTOPLASMIC (POTENTIAL).
                                                                                                                                                                                                                          478 AA.
                                                                                                                                        0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        InterPro; IPR001478; PDZ.
InterPro; IPR001478; PDZ.
InterPro; IPR001264; Ser_protease_Try.
Pfam; PF00089; trypsin; 1.
Pfam; PF00895; PDZ; 2.
PRINTS: PR00834; PROFEASES2C.
SMART; SW00228; PDZ; 2.
PROSITE: PS50106; PDZ; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               CATALYTIC.
PDZ 1.
PDZ 2.
                                            POLY-SER.
POLY-SER.
                                                                                                                                                                                                                          PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         EMBL; AP001118; BAB12943.1; -.
                                                                                                    47713 MW;
                                                                                                                               100.08;
                                                                                                                                        9; Conservative
                                                                                                                                                                                                                          STANDARD;
                   44
67
1108
1152
1179
2009
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      478
254
372
469
133
238
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  MEROPS; S01.273; -
                                                                                                   449 AA;
                                                                                                                               Best Local Similarity
Matches 9; Conserv
                                                                                                                                                         160 GIGFAIPSN 168
                                                                                                                                                                     316 GIGFAIPSN 324
           Complete proteome
                                                                                                                                                                                                                                                                                 DEGP OR BU228
                                                                                                                                                                                                                         DEGP_BUCAI
P57322;
                                                              DOMAIN
ACT_SITE
ACT_SITE
ACT_SITE
SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ACT_SITE
ACT_SITE
ACT_SITE
                            TRANSMEM
                                                                                                                     Query Match
                                     DOMAIN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               SIGNAL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                DOMAIN
                                                      DOMAIN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          DOMAIN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   DOMAIN
                                                                                                                                                                                                                           KW
FT
FT
FT
SO
SO
                                                                                                                                                          ò
                                                                                                                                                                           qq
```

```
This SWISS-FROT entry is copyright. It is produced through a collaboration the between the Swiss Institute of Bioinformatics and the EMBL outstation the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to licenseelsb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Thao M.L., Baumann P., "Sequence analysis of a DNA fragment from Buchnera aphidicola (Aphid endosymbiont) containing the genes dapD-htrA-ilvI-ilvH-ftsL-ftsI-murB.";
                                                       ;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ;
0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   POTENTIAL.
PROBABLE SERINE PROTEASE DO-LIKE.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       CHARGE RELAY SYSTEM (POTENTIAL).
CHARGE RELAY SYSTEM (POTENTIAL).
CHARGE RELAY SYSTEM (POTENTIAL).
C044824F/FE44E98E CRC64;
                                                                                                                                                                                                                                                                                         DEGP_BUCAP STANDARD; PRT; 478 AA.
085291;
16-OCT-2001 (Rel. 40, Created)
16-OCT-2002 (Rel. 40, Last sequence update)
15-JUN-2002 (Rel. 41, Last annotation update)
Probable serine protease do-like precursor (EC 3.4.21.-).
DEGP OR HTRA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                2.3%; Score 9; DB 1; Length 478; 100.0%; Pred. No. 0.34; 1ive 0; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Buchnera aphidicola (subsp. Schizaphis graminum).
Bacteria; Proteobacteria; gamma subdivision; Buchnera.
NCBI_TaxID=98794;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Curr. Microbiol. 37:214-216(1998).
-!- SIMILARITY: BELONGS TO PEPTIDASE FAMILY S2C.
-!- SIMILARITY: CONTAINS 2 PDZ/DHR DOMAINS.
2.3%; Score 9; DB 1
100.0%; Pred. No. 0.3
:ive 0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Repeat; Signal.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          CATALYTIC.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               MEROPS; SO1.273; -.
InterPro; IPRO01478; PDZ.
InterPro; IPR001940; Protease2C.
InterPro; IPR001254; Ser_protease_Try.
Pfam; PF00089; trygsin; 1.
Pfam; PF00595; PDZ; 2.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        SEQUENCE FROM N.A.
MEDLINE=98353428; PubMed=9688822;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  EMBL; AF060492; AAC32331.1; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            51303 MW;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                PRINTS; PRO0834; PFOTEASES2C.
SMART; SM00228; PDL; 2.
PROSITE; PS50106; FDZ; 1.
Hydrolase; Serine protease; F
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              9; Conserwative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            478 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Best_Local Similarity
Matches 9; Conserv
                                                                                                                                               113 RALGSGVII 121
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   118 YENFIQTDA 126
```

```
This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation her Buropean Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
                                                                                                                                                                                               STRAIN-Malish 7;
MEDLINE-21442074; PubWed=11557893;
Ogata H., Audic S., Renesto-Audiffren P., Fournier P.-E., Barbe V., Samson D., Roux V., Cossart P., Weissenbach J., Claverie J.-M.,
                                                                                                                                                                                                                                                                          "Mechanisms of evolution in Rickettsia conorii and R. prowazekii.";
Science 293:2093-2098(2001).
-i- SIMILARITY: BELONGS TO PEPTIDASE FAMILY S2C.
-i- SIMILARITY: CONTAINS 2 PDZ/DHR DOMAINS.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Repeat; Signal; Complete proteome.
POTENTIAL.
PROBABLE SERINE PROTEASE DO-LIKE.
CATALYTIC.
PDZ 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            CHARGE RELAY SYSTEM (POTENTIAL).
CHARGE RELAY SYSTEM (POTENTIAL).
CHARGE RELAY SYSTEM (POTENTIAL).
                                                                                                      Rickettsia conorii.
Bacteria: Proteobacteria; alpha subdivision; Rickettsiales;
Rickettsiaceae; Rickettsieae; Rickettsia.
NCBI_TaxID=781;
                      15-JUN-2002 (Rel. 41, Created)
15-JUN-2002 (Rel. 41, Last sequence update)
15-JUN-2002 (Rel. 41, Last annotation update)
Probable serine protesse do-like precursor (EC 3.4.21.-).
DEGP OR HTRA OR RC0166.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        DB 1; Length 508; 0.36;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            D2F53A690ECD0AD7 CRC64;
508 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        2.3%; Score 9; DB 1
100.0%; Pred. No. 0.3
iive 0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                             EMBL; AE008583; AAL02704.1; ALT_INIT.
InterPro; IPR001478; PDZ.
InterPro; IPR001940; Protease2C.
InterPro; IPR001254; Ser_protease_Try.
Pfam; PF00089; trypsin; 1.
Pfam; PF00595; PDZ; 2.
 PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          55599 MW;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         PRINTS; PR00834; PROTEASES2C.
SMART; SM00228; PDZ; 2.
PROSITE; PS50106; PDZ; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Aydrolase; Serine protease;
STANDARD;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               119
286
413
134
164
242
508 AA;
                                                                                                                                                                                   SEQUENCE FROM N.A.
DEGP_RICCN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 DOMAIN
DOMAIN
DOMAIN
ACT_SITE
ACT_SITE
ACT_SITE
SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    SIGNAL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    CHAIN
```

Search completed: November 18, 2002, 11:35:28

ö

Gaps

; 0

0; Indels

9; Conservative

Matches

160 GIGFAIPSN 168

ò

Local Similarity

Job time : 14 secs